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KIM MARSHALL

MANAGER EXAMINATION SUPPORT AND



AUSTRALIA

Patents Act 1990

CSL LIMITED

PROVISIONAL SPECIFICATION

Invention Title:

P. gingivalis sequences

The invention is described in the following statement:

P. gingivalis sequences

FIELD OF THE INVENTION

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The present invention relates to *P. gingivalis* nucleotide sequences, *P. gingivalis* polypeptides and probes for detection of *P. gingivalis*.

BACKGROUND OF THE INVENTION

Periodontal diseases are bacterial-associated inflammatory diseases of the supporting tissues of the teeth and range from the relatively mild form of gingivitis, the non-specific, reversible inflammation of gingival tissue to the more aggressive forms of periodontitis which are characterised by the destruction of the tooth's supporting structures. Periodontitis is associated with a subgingival infection of a consortium of specific Gram-negative bacteria that leads to the destruction of the periodontium and is a major public health problem. One bacterium that has attracted considerable interest is P. gingivalis as the recovery of this microorganism from adult periodontitis lesions can be up to 50% of the subgingival anaerobically cultivable flora, whereas P. gingivalis is rarely recovered, and then in low numbers, from healthy sites. A proportional increase in the level of P. gingivalis in subgingival plaque has been associated with an increased severity of periodontitis and eradication of the microorganism from the cultivable subgingival microbial population is accompanied by resolution of the disease. The progression of periodontitis lesions in non-human primates has been demonstrated with the subgingival implantation of P. gingivalis. These findings in both animals and humans suggest a major role for P. gingivalis in the development of adult periodontitis.

P. gingivalis is a black-pigmented, anaerobic, asaccharolytic, proteolytic Gram-negative rod that obtains energy from the metabolism of specific amino acids. The microorganism has an absolute growth requirement for iron, preferentially in the form of haeme or its Fe(III) oxidation product haemin and when grown under conditions of excess haemin is highly virulent in experimental animals. A number of virulence factors have been implicated in the pathogenicity of P. gingivalis including the capsule, adhesins, cytotoxins and extracellular hydrolytic enzymes. In

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particular, proteases have received a great deal of attention for their ability to degrade a broad range of host proteins including structural proteins and others involved in defence. The proteins that have been shown to be substrates for P. gingivalis proteolytic activity include collagen types I and IV, fibronectin, fibrinogen, laminin, complement and plasma clotting cascade proteins, α_1 -antitrypsin, α_2 -macroglobulin, antichymotrypsin, antithrombin III, antiplasmin, cystatin C, IgG and IgA. The major proteolytic activities associated with this organism have been defined by substrate specificity and are "trypsin-like", that is cleavage on the carboxyl side of arginyl and lysyl residues and collagenolytic although other minor activities have been reported.

P. gingivalis trypsin-like proteolytic activity has been shown to degrade complement, generating biologically active C5a, impair the phagocytic and other functions of neutrophils by modifying surface receptors, and abrogate the clotting potential of fibrinogen prolonging plasma clotting time. The trypsin-like proteolytic activity of P. gingivalis also generates Fc fragments from human IgG1 stimulating the release of proinflammatory cytokines from mononuclear cells and is associated with vascular disruption and enhanced vascular permeation through the activation of the kallikrein-kinin cascade. P. gingivalis spontaneous mutants with reduced trypsin-like activity as well as wild-type cells treated with the trypsin-like protease inhibitor N-p-tosyl-L-lysine chloromethyl ketone are avirulent in animal models. Further, it has been shown that P. gingivalis grown under controlled, haemin-excess conditions expressed more trypsinlike and less collagenolytic activity and were more virulent in mice relative to cells grown under haemin-limited but otherwise identical conditions. The increased expression of the trypsin-like activity by the more virulent P. gingivalis has led to the speculation that the trypsin-like proteolytic activity may be the major determinant for infection or disease.

There has been considerable endeavour to purify and characterise the trypsin-like proteases of *P. gingivalis* from cell-free culture fluids. Chen *et al*, (1992) [J Biol Chem 267:18896-18901] have purified and characterised a 50 kDa arginine-specific, thiol protease from the culture fluid of *P. gingivalis* H66 designated Arg-gingipain. A similar arginine-specific thiol protease has been disclosed in JP 07135973 and the amino acid sequence disclosed in WO 9507286 and in Kirszbaum *et al*, 1995 [Biochem Biophys Res Comm

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207:424-431]. Pike et al (1994) [J Biol Chem 269:406-411] have characterised a 60 kDa lysine-specific cysteine proteinase from the culture fluid of *P. gingivalis* H66 designated Lys-gingipain and the partial gene sequence for this enzyme was disclosed in WO 9511298 and fully disclosed in WO 9617936.

In order to develop an efficacious and safe vaccine to prevent P. gingivalis colonisation it is necessary to identify and produce antigens that are involved in virulence that have utility as immunogens to generate neutralising antibodies. Whilst it is possible to attempt to isolate antigens directly from cultures of P. gingivalis this is often difficult. For example as mentioned above, P. gingivalis is a strict anaerobe and can be difficult to isolate and grow. It is also known that, for a number of organisms, when cultured in vitro that many virulence genes are down regulated and the encoded proteins are no longer expressed. If conventional chemistry techniques were applied to purify vaccine candidates potentially important (protective) molecules may not be identified. With DNA sequencing, as the gene is present (but not transcribed) even when the organism is grown in vitro it can be identified, cloned and produced as a recombinant DNA protein. Similarly, a protective antigen or therapeutic target may be transiently expressed by the organism in vitro or produced in low levels making the identification of these molecules extremely difficult by conventional methods.

With serological identification of therapeutic targets one is limited to those responses which are detectable using standard methods such as Western Blotting or ELISA. The limitation here is the both the level of response that is generated by the animal or human and determining whether this response is protective, damaging or irrelevant. No such limitation is present with a sequencing approach to the identification of potential therapeutic or prophylactic targets.

It is also well known that *P. gingivalis* produces a range of broadly active proteases (University of Melbourne International Patent Application No PCT /AU 96/00673, US Patent Nos 5,475,097 and 5,523,390), which make the identification of intact proteins difficult because of their degradation by these proteases.

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SUMMARY OF THE INVENTION

The present inventors have attempted to isolate *P. gingivalis* nucleotide sequences which can be used for recombinant production of *P. gingivalis* polypeptides and to develop nucleotide probes specific for *P. gingivalis*.

In a first aspect the present invention consists in an isolated *P. gingivalis* nucleotide sequence, the nucleotide sequence consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO. 1284 and sequences complementary thereto.

In a second aspect the present invention consists in an isolated *P. gingivalis* polypeptide, the polypeptide being at least partially encoded by a nucleotide consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO. 1284 and sequences complementary thereto.

In a third aspect the present invention consists in a nucleotide probe specific for *P. gingivalis*, the probe including a detectable label and a nucleotide sequence of at least 15 nucleotides, the nucleotide sequence being derived from a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO. 1284 or a sequence complementary thereto.

DETAILED DESCRIPTION

Preparation of the P. gingivalis library for sequencing.

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To determine the DNA sequence of *P. gingivalis* genomic DNA was isolated from *P. gingivalis* strain W50 (ATCC 53978) essentially by the method described by Mamur J. (1961). Cloning of DNA fragments was performed essentially as described by Fleischmann *et al.*, (1995). Briefly, purified genomic DNA from *P. gingivalis* was nebulized to fragment the DNA and was treated with Bal31 nuclease to create blunt ends then run twice on preparative 1% agarose gels. DNA fragments of 1.6-2.0 kb were excised from the gel and the DNA recovered. This DNA was then ligated to the vector pUC18 (*Sma*I digested and dephosphorylated; Pharmacia) and electrophoresed on a 1% agarose preparative gel. The fragment comprising linear vector plus one insert was excised, purified and this process repeated

to reduce any vector without insert contamination. The recovered vector plus insert DNA was blunt-ended with T4 DNA polymerase, then a final ligation to produce circular DNA was performed. Aliquots of Epicurian Coli Electroporation-Competent Cells (Stratagene) were transformed with the library DNA and plated out on SOB agar antibiotic diffusion plates containing X-gal and incubated at 37°C overnight. Colonies with inserts appeared white and those without inserts (vector alone) appeared blue. Plates were stored at 4°C until the white clones were picked and expanded for the extraction of plasmid DNA for sequencing.

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DNA sequencing

Plasmid DNA was prepared by picking bacterial colonies into 1.5ml of LB, TB or SOB broth supplemented with 50-100ug/ml Ampicillin in 96 deep well plates. Plasmid DNA was isolated using the QIAprep Spin or QIAprep 96 Turbo miniprep kits (QIAGEN GmbH, Germany). DNA was eluted into a 96 well gridded array and stored at -20C.

Sequencing reactions were performed using ABI PRISM Dye Terminator and ABI PRISM BIGDye Terminator Cycle Sequencing Ready Reaction kits with AmpliTaq DNA polymerase FS (PE Applied Biosystems, Foster City, CA) using the M13 Universal forward and reverse sequencing primers. Sequence reactions were conducted on either a Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) or Hybaid PCR Express (Hybaid, UK) thermal cyclers. Sequencing reactions were analysed on ABI PRISM 377 DNA sequencers (PE Applied Biosystems).

The sequences obtained are set out below.

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It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Dated this 31st day of December 1997

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CSL LIMITED

Patent Attorneys for the Applicant:
F.B. RICE & CO.

References.

Mamur, J. (1961) A procedure for the isolation of deoxyribonucleic acid from micro-organisms. J. Mol. Biol. 3, 208-218.

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Fleishmann, R.D. et al. (1995) Whole genome random sequencing and assembly of *Haemophilus influenzae* Rd. Science 269, 496-512.

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 610 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...610
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

gagcataccg cccggccagc gttctaccac atagggcatt cccactgatt ggccaattcg 60 gcgataggtt ctttggcctg cttcttcgtg gcaacgaaag aatcttcttg ccatttttgg 120 ccataccett aataacttcg getgettgte tactttagea aetgttttgt geaggtegat 180 240 aatatgaata tegttggete cataaagata taeggageea taageeggat teeaetttet 300 cttgagtgtc cgaagtgagc accggcttcc aataattgat caaaagaaat tcttacattt 360 togtttacgt totttgtaat gattactgtt tgcaatccaa accgtagage agactcgaaa 420 agaaatgaat tacccccgaa tgcaatccga tgatttagat actaaacgcg agaaatatcc 480 tctaaggaca ttaacgctta cgaattggaa tctcttgcga gctttgggac gtcccggttt 540 cttacgttct ccacgegagg ategegagtg atgaageett etgaaegeaa agegggtttt 600 cgtccggatt gatcttgacc agtgcacggg ccgatagcca agcgagcact cgttctgacc 610 tttgaaacca

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 676 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...676
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

```
ccctcgcgtt tgcaacaagt ccgccggaca gaacctctcc cgtaccggat ctgagcgaca
                                                                       120
tgattgcaga agtggaattg gcacgcaagt cctgaccgaa ctgcaatatc gccgattgga
                                                                       180
                                                                     . 240
tottttcaca tatagogtac ggaattggag cotttcgcac cggattattc ctatataaaa
ccacagacat tcagctcatc gatgggggag ccttatccga cagaataatc atgcggaaaa
                                                                       300
aatccgcgga atcgaactca aaccccgcta ctggtttttc agctggagac aatgctgcag
                                                                       360
                                                                       420
ttctcacaga actacatttc cgaaaactgg taaaaggagg atcgagcaac ctgaatatca
                                                                       480
tgttcggcaa tctgatcgtc cccaatatcg caataagaag attcgctgga aaaatgagtt
                                                                       540
ggaaaacaaa taagtgtett caatgeagee aaagacaegg teaategeta tegagtggeg
aggatttgct ccgcctgcgt tccaacttcg gctataaggc tttcaagcgt ggtactactc
                                                                       600
tttcgatgcg gaaatgcgta cacagctatt taccaatgag ctgaaaacag cctaaaaaaag
                                                                       660
                                                                       676
caatctgcat tcctgc
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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...999
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

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60
ggcataataa atcaatccgc acttcggaca cgatttggct ttcgggtttt ctccgcaaaa
ccatcgtttc cgcagcgcgg acagtatctg aaaggtgcag cggatgctca gcgtttattt
                                                                       120
tgcctcccat cccaaagcac ttgccccage acageggcat egetetett gagetgagag
                                                                       180
                                                                       240
aagagcagct tggtctccct cggtagatat tcagcacatt cttttccatg tggtggcgga
                                                                       300
teggateate ageaggteae etgetttggt aagaceaeeg aagaggatga tegeteegga
                                                                       360
ctggagaagg taacgaagtc ggcaaaagcc tctccgagga tggtcccgta gtctcgaata
                                                                       420
totottgago aaggocatog coactgatag otoatogtaa acatotttog aagtgattag
                                                                       480
ategggetga atgtteegga gaagetettg teegaaegga tgteeaggta ttegegaget
                                                                       540
gtacgggcta teetgtagea gaggtgtaag tetegagaea gecetatetg ecacaacega
                                                                       600
catgcgacca ttgcggcgaa cgatcatgtg tcccagctca ccggcaaacc atcgtgtccg
                                                                       660
tacaccaage tgecattgae tactatgeeg etteegaeee egtaeegage gtgataaega
                                                                       720
tgaagteett catgeeacga getgeteata ggteatetet eegatggeag cageattgge
                                                                       780
atcattggtc agtgtgtggg gatacctaat gaatcggtga gcatttgggc gaagggtatt
tgggctgttt ccaaggcaaa ttgggcgcaa actcgatcga tccggtataa tagttccatt
                                                                       840
                                                                       900
gggagcacct acaccgatac cctttatctt ctctttccct ccacctgttc aatcaactga
                                                                       960
ttgatgccgg cagtcagatc tttgatataa tgntcagatc gttgtgcgct ccggtcttga
                                                                       999
tggacgaact tataaccaaa tgccacgagc gtccaccac
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 658 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...658
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

tagactacct	gacgataccc	gtacaggcgg	aatacaatat	gctcaaggaa	ggctgaagct	60
acacagaagt	ctctatacgt	ccctgctgct	ggagagttct	teegegtgat	catcgacggt	120
acgatggtct	atgacgatcc	caagctggaa	cagcgcagat	ggatctgcgc	gaactgaact	180
teteggacaa	gataaaggag	cggatttcgg	tgtcataata	ggagccgact	attatttcgc	240
gcgacgatag	gtgcgtttgc	cgatgtcaca	ttcggcctga	tecetetgae	gggtcacact	300
tcaaggctat	teettacegg	atgtataacg	tettegeacg	tatggatttt	cctacagact	360
caattactga	gccactacac	acggatcgcc	tgccggtctt	cgttggctct	ttcaaaaact	420
atcactcttt	caacacctcg	agcatagtac	aatacaaata	caatggaatc	gataacccaa	480
atatatogca	cggctacggt	ccqaqcaqta	gccacacgat	tggcccacgt	cgggctgcta	540
gatgnttctc	gateggaace	cccgggcgac	ctctttccgt	gttacgctta	cggcaagcct	600
tgcttgccac	gggcaaagga	cacctcacgg	atgcagcatc	ttgccgcttg	gaagcaag	658

- (2) INFORMATION FOR SEQ ID NO:5
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 628 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...628
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

tetteegett	tttttggaat	actcattcgc	atcgaaagct	ctacagagct	caaggatgcg	60
			tattttgcga			120
			gcgtctatct			180
			aacaaagtgt			240
			cggtggcaac			300
			acggaaaacg			360
			cttgcccaat			420
			gagtccgagc			480
			aggcgaatcc			540
acacaacaaa	tagtaggeta	caattcaaaa	gtgatcatca	tqcacaqaqq	atatatcatc	600

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 970 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...970
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

60 gacttottta cocogotaaa agtaacotta otgatgogag gacgttoagg acaatgattt tcagatagac tttattgccg acatatttat ccgcgatgtt cgcacatttg agaagtagcc 120 ctgacgcata attctattca, cggcagcgac atggcatctc caggaatcag gacttcatca 180 240 cctacagcca agcctgaaga ttgcgcaaga caaagtcatc gaaagacctc attccctcga 300 totoatagat gotatggtot tatgaatagg ottggoatag gatatttoag ggottatata tggatctccg tgaggggtca gatccgagga ctgtcctttc aggtccctat gctggcgcag 360 420 aagagagetg etaeggeaat aatetttttg taatagtett teteaaatga tteaatattt attttctctg agagegattt gtegetggte ttgeegaate gaegeteeet egatgaatat 480 540 tottotatgg tgccttcaga cagtcggcat caaagtccgg ccaaagcgta tcggtaaaaa caattccgta taggccattt gccacataag aaaatgctga tacgcttcct ccacctgtac 600 660 gaatgaagag atccggatcc ggaatgcccg cggtggaaga tgatcagaaa ccaaatcgac atttatatct tcaggctcca cacttcatcc cgaacctttc gagccaatct acggatgaca 720 toggtoattt cocaggagaa otgtagotaa gggocaaaac caaagtoago cocgtgttto 780 840 cggcgtctct cgaataccct tttctaacga ttcacggaca tcctcgggga gccactgaaa 900 togoogatag coaagaggog aatgttattg gtcatcaagt cogcatotca ttcatgataa 960 gctgtaacga aaaggcccat cagcgccctg attcctcttt cggacgattc caattcttcg 970 tactgaaagg

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

agaaccagaa gtatcgaacg aaggaaacaa tcaaatgata tcatctccca aaggtttttc 60 aaaccctcga aagaggaaat aatataatcg gtgcagggtt ggaaaggtat tcctttctga 120 ccatcaggac ggttgtaaat cccagttccg tcctgctttt atttcggaag cgggatcatc 180 240 qcctqccaca taggctttcg gtctattaag ttcggttctc tatgctgact gtgataaaga ttatcggaca aaatagagtt ctatcctcct gtagaatgta taaaggattg ggagacgact 300 360 aggetgettt geaggaatet tttatttaeg gaaacaaaat ttetteggae aacttttget 420 tegeattaaa gaatteeage agegatteeg aatateggea caaegggeaa gtagaaagtt tttgcaaaat attctacttc caagggcgta atcgttttcc atattatctc tcaaaaggtc 480 540 tctcaagccc cgaaagagga aataatataa tcggtgtagg agttgggaaa ggtattcctt 549 ctgaccatc

(2) INFORMATION FOR SEQ ID NO:8

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

agccgcacga	ttggaaaaga	aactggagca	actcacagcc	taacggcgca	gagcctgtgc	60
			teeggateee			120
gattctttc	ggatacgatc	agtagcagtc	tcccacttgc	aagtgcatac	gccctttcgg	180
tacacgataa	gccctccctc	ttcgtaccag	gatgacaagc	tcttcatcac	gaagagaaag	240
			gaagcatcca			300
ttcccgtctc	ttccggtatt	tccacaccga	acaggctacc	tatggcggcg	aaggaatatc	360
cagtccgagc	caacgtgcta	cctgggagat	cgactcccct	gtacgagcag	agagagtatg	420
			ccgctccggg			480
aggtggcaaa	atgataggaa	eggeteegeg	caatccgacc	cagctgagaa	aggtcttacc	540
ctgaatgata	ttttgcggaa	gggaatcagg	cagaaa			576

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

gctttcatct	ctattctcct	tttttattct	attgtgtttt	tttcatattc	tcttcggaca	60
tagccgtttc	cgcatacaag	gcttcctctt	cccatccggc	atttccacaa	actccccctc	120
cgcatcagcc	ccgcgatcga	gacaatatcc	aatagctcca	tggcgtaggc	cgtttcccgg	180
acggcttcgt	cccgatgaga	gcgatcccgt	tectgttgga	cgaaagtcgt	cccaccgtat	240
				caagctacag		300
accaaccgaa	gcgacaaccg	ccttgaagga	tgccggacac	gatctcccaa	ctcgccatct	360
tttccaagag	aactttgtcc	gaatcatctt	cctngcccgt	ttcacgctca	ggaagaccga	420
tcaaagcccg	caaaagctgc	agtccgaatg	atagggagcc	ggatccggca	atcccttcag	480
caagcaatac	gctccaactc	ctcttgcgga	aaatggtacc	ggcataaaaa	ctttncagtg	540
ccggtcgatt	ttattctctc	ttacgcatca	tcttatcacc	tcctagct		588

- (2) INFORMATION FOR SEQ ID NO:10
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...473
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

aacacaaaac	tttagaaggg	agtcttacac	ttcgtcccat	cgagtgtctt	cctttaccgg	60
tagtttcatg	agtggcaaga	ccgctgccct	gaatgatgtc	ccatcaaaat	caatagcaaa	120
				tgtaggaggt		180
				aaagacgatg		240
taaggetttt	acgtcacagg	ggtaggacga	ttgttcaaaa	acctcgatat	catcgatcat	300
				atataccgcc		360
				attgagcaat		420
				gcattctgac		473

- (2) INFORMATION FOR SEQ ID NO:11
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...625
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

tettattata gaatttgatg atttegttaa teatttettt eteeteeggt eteeteegt 60 agtggtgagg gctaccgctt tcgagagctc atccacggca tatcgtattt cttcttgctg 120 atacctetgg taacgatgee ggtactttga ceageaattt tgaaaaeggt gacaatatet 180 tatagataac ggacatgctg cagcagaaaa gcgcgagtat tgcagcggat tcttccgcgc 240 atacatttcg gcagaatctc ttcgaacagc aaaaggacca gtggccagga gtatgtctgg 300 atcagaaatc caatgatcgg agaagagaaa acgaatgtct gctgatggca taattggaaa ggataacgat ggctacatta atcacattat teegateaga atagtageta atagetgatt 360 420 egaattgtet aataaattgg aagegegatg teggaagagt gatteegtte geggatgtte 480 tgcagatcga cggctttagt gaaaaataag ccacctcaca ggaggacata aaagccgaaa 540 gcaaagaaga agcaggtcga taatgaaagc cactatggct gctgcaccat aggatgaccc 600 gaageeette aaaaaateag tataa 625

- (2) INFORMATION FOR SEQ ID NO:12
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...622
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

ggggatttgg	ggcaagataa	gttactttgt	agagettgaa	tagcaaacag	ggatttctgc	60
ctattttcca	aaaatctgca	teateastta	++~~~~~		ggacccccgc	
annantttat	tataattaa	cegeegaete	ccyaaacggc	tgagagccaa	cgggggcgca	120
uggugeeege	couggingge	cacccgagag	cttcgtctcc	ggggagagtt	ttaattatct	180
tatcgggcaa	cttaaagcag	ctatcagttc	ttgagcatga	Cagagttgta	tgatcagagg	240
ctaaaatagg	Сасавадава	aaaataaaa		augugeegeu	cgaccagagg	240
2000000	Judauagaaa	ggcgccaagg	acactcataa	gcccgaaaca	cctgcccaga	300
ayyaccatct	ccagagggac	ctgaagctgg	tttgtaatta	gttatagaag	ctcaccccag	360
				- , ,		200

			tastatatta	ttatttaatc	attacgaccc	420
tagaggtagc	gagttttgct	ggggrgagrg	Caccegeta	1	+++++=0000	480
aatagatggg	tattatcaaa	atccatatta	gatatgctta	atgcaattta	tttttaccga	
	ant+tatent	catcatatco	cgatattgcc	aaagttaatc	acattgctct	. 540
ttgtctcall	gottatege			tagggaaga	totaagttog	600
cttcctcatt	tataatagca	agatacctcc	teageraaya	caggeddaga	tctaagttcg	622
gtatggaggg	ataagtgttg	tg				022

- (2) INFORMATION FOR SEQ ID NO:13
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 605 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double(D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...605
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

agcagccggc cggccaacgg aaagcttcgc cccccatggc ggcacgaata tttcgataga 60 cacgtaagaa gggctttgga aagacgagcg accacgtact tgataatgtt ggctccccc 120 ttcacgacac gctgtttcag ttctgccact gctcgttggt cagcttgtcg gtaccgatca 180 gateggteag aggegteegt ttacettgge egtgetggeg aaaacageea tetgetegee 240 atgactccat aagtacgcgt gttggtcacg agactttgtt tgatgccgaa gtgctagcca 300 gttcgctttg cagacgtgtg ctgtccaaac cggccaaagt agtacctgcg aaggcttcag 360 cccggagtag ataagcgtaa caagaccggt gagtcagccg gattgaagat gatgatcacg 420 tgcttacagt cgggacaata gtcttgatgt ccttgcccag ctgagcagcg atttcggcat 480 tgcccttgag agatcctcgc gggtcatacc ctctttgcgc ggagcaccgg ccgaagaaat 540 atatatttgg catctgtaag agcetettga tgtengatgt aaaagteaat teaggeette 600 605 gaatc

- (2) INFORMATION FOR SEQ ID NO:14
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 590 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

60 gggttetece ttgtegeeca tegtactega tgaagagaga aaggegatae tegteatatg 120 cgcaacaacg gcttctggaa gttctccgcc gaggatgtta ttatgaagca gatactaccg tttcaggagg atcgggtacg aaatctgcga tctgaaatta gtggtcaatg gcatcgggcg 180 ttatccatat cggatcgcag ggtattcttt catgcccgat tatgatcctc tcgaatcgga 240 cttcaagttc aggagctgcc acgtatcgat tcgatttcgc gtggcgatta cacttttact 300 atgggagtag gggacgttat atccgggcat cggctctcac gcgtcggtgt ccgttacacc 360 gggagetttt ttetgegagg atgatgtgga acetettata teaagetgaa tgegeteeet 420 atcgttcgga acgtgaatat cgatttgtgg agcacaatgg taaggatgag attgctctgg 480 eggatagete egeettgtgg actgetatat tettacegtt eeggeeaaga geaaategte 540 590 gaageegaag teeteggeae caatteeget ggagaetteg gggeggettg

(2) INFORMATION FOR SEQ ID NO:15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...522
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

cctgagccac acactggtct ataatggcat tggacacttc ggccagacgt atacgttggc 60 ctcgcgagca cgatagtcac ctcctttgat cgtatcgtga agagtcgata aacggagtcg 120 ccgtcgttct ggtagttctt ggcggcatga tacctccctg tgcagcgatg gagtgcgcac 180 ggcgaggaga atcctgatgc agaagttaag cacattgaag cccatctcgc cgaaagaagc 240 agcagegaag caceggeeag geeggtaeeg accaegataa tateeagaeg aegttgttgg 300 ccgggttcac cagettctga tgatcettat agttggtcca etttetttca gcgggccggc 360 gggtattttg gaatttattg tagccatagt gaaatacttt gaattagggt gtactatcaa 420 ccgatgaatg cctgacaagc aatactatca ggaccaaagc gaaaccgcct accaatacgg 480 agaaaccaca tagagatgca cttgacacga ttcatccaga tg 522

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 617 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...617
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

gatagttgat	caagttctta	ccggggaagt	tcttcgtacc	gttgaaagca	tgtgttccaa	60
gaagtgagcc	aaaccggact	ggctatcttc	ttcaagaaag	aacctacctt	ttgtgcgata	120
aagaaatccg	cacgatcttt	cgggttccgt	tgtgacggat	gaaataagtc	aatccgttgt	180
ccaacttacc	gacacgacag	ccggatctgt	agggagtggc	tgagcctgtt	gggcagaaag	240
cttcacggaa	tgaatcccac	aagcagaaga	ccaagtgata	aaaatctttt	caatccatat	300
aggtatctaa	ggttactggt	ttggttatta	agtaatttcg	gccaaagtac	ggttttttca	360
tcggattagc	acttttcaat	ccggctgtat	gtcggaaaaa	ccgtgagagt	cccactttac	420
aggaccggtc	tctatacttg	gtcgaaaaaa	caaaatgacg	cacacgcttt	tcgcagggaa	480
taacagagca	aaaagaggca	cgactctccc	gagcggtgcc	tccttcaaaa	acatgagata	540
gataattact	tcgtttctat	atgaatgtga	tcctcagtaa	ttcgtttctg	gctcgaagta	600
agcctgcgga	tgagcgc					617

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 587 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...587
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...5\overline{63}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

aatatatcga aaagagttct gagggtttga tggagttggg catgatgcgc ttgtcatctg cttgteggat gaegataage etgteggtge gatagategt atgagtaega tgeettteat 60 cgacgtgtag ccgtagggtt attcgttttc ccgaataccg tcggctggga atagccgtcg 120 agteteteeg caagatteee attatgtttt agactatntt acgettgeat cagateateg 180 cttattgctg gaagataaca agccgagccg gatgctgttc gaagctgccg gcttgagcat 240 acagecacce teegecaatg gatgtggeat geeggegatt atttgatgtt ttgetttate 300 agttatggaa aagatagtte cecetgetgt ceaatagaag agetgegeeg cattetgegt 360 gagcacgaat acaggtatta cttctctcat ctccgactat cgatgacttc gagtatgacg 420 ccatgatgaa cagcttgagg agctggaacg ggaatacccc gaatgggata gtcctgactg 480 540 cctacgcatc gtgtcggaag cga 563

- (2) INFORMATION FOR SEQ ID NO:19
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 954 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...954
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

gaaccatton	taacqqaqtt	at a				
taaccaacca	tadegeage	cregageage	catctcgatc	gaaatcgacg	ctcgcgagca	60
	- Judgaagee	gateedataa	adcadaacto	72~a+		
J	Juneoucut	CHULCUCACC	CCECGGaggt	72222++		120
accgtctcat	accccatted	CCCaatacca	222334	gaaaattgca	grgrgccgcc gcacctccgc	180
tgagacgacc	2412222	egeaacacyc	agagcagagc	caccgagtcg	gcacctccgc	240
	J J	9900000000	CCCCCAACAC	ttooaat		300
	g - c u g g g u	aacccccatc	LEGELGLGAA	tattosooo		
gcccggccat	cctgccgatg	GAAAAaa+++	ataasst	caccagggg	gaaaatatcg	360
	5 - 5 - 5	Januadattt	Ccyyaaatga	agaggetett	tatccgaata	420

agccgaatgc	taccataaaa	caagagagaa	ctctcqtcct	ctctcatcag	tectgeegge	480
atctccgaag	anaccanacc	ttatctcgga	aaacttatgc	acctgtgaac	ccgaagcatg	540
accggaagcg	agecgaact	acaccaacct	cttactcttq	gggagettat	geteceattt	. 600
cgggatcgac	aadaccgcct	ccaceatett	cacagacata	attttttcc	gaagettgae	660
egggategae	thetacaga	asstatatta	aaggaggggg	cgcaagcatc	acgetetacg	720
gtccagctgc	ttetgaggag	taggerage	ttataataca	cttgaaagcc	atcagcaggc	780
ggcaccacgg	ccaagegrug	Lgegeageet	-ttttagargeg	agtttatatt	cctttactta	840
gcggtcgatc	ttggcttcga	gettettege	ettttegege	agececeee	ctatectet	900
gtctcggcaa	tgatggtatc	cagttcgccc	gegeeeeg	theresta	ctatgctctt	954
cagcacctct	tcagagtagc	tatatcggtc	tegetgtgga	ttegaegtgg	accc	754

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 598 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...598
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

taacgctctg	gacattccgc	tctatctgag	aatcgctaac	gaattgtatt	gaagcgtctg	60
atcgtgggcg	gtttcgatgg	tatatataa	ttcaqccgaa	tttccgaaat	gaggggatgg	120
accgcacgca	taatcctgag	ttcacacat	ggagatetat	gtggcgtata	aggattacaa	180
atagetaeta	aactttcaaa	gcagatgctc	gaacgcatct	gtatggatgt	gctgggtact	240
ecggacgacg	aataaaaaa	aaattgatcg	acttcaaggc	ccctacaaq	cgaggaccat	300
acteaatyaa	ggcgggcggg	atacqqqtat	cgacatcage	ggatgaacga	ggccgagctg	360
cgtcaggtat	acceatgage	acacateasa	caaatgaaac	gatggggaaa	ggcaagetea	420
egteaggtat	gegaeaaget	gggcgcagag	gaactatatc	cagoctactt	tcatcacaga	480
tcgatgagat	ctteggegag	agtgegagaa	gaaccacace	ccaatccaga	tcatcacaga	540
ctatccgaaa	aaatgtcgcc	tetgaegaag	gageacegea	ataataaaa	gctgacagac	598
gattcgagct	gatggtcaat	ggcaaggagt	tggccaacgc	ccacceggge	cyaacyac	370

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1349
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

cagatatttc tgcaaacaaa tcagttccca aaatgcggaa agcttgacgg tactgaaaaa 60 agttgacagt tgggcgggat gcaaccagta tccattatgg caaacattta aacaactttg 120 aacgccttag catccttgag gattaccctc ggggtcagat agcaaagtag ccattgagca 180 gaaatatggt ctaagtatgg tctcattcgc tcttggctta gtaaatttgg actcgaagat 240 aaagtcatcc agtcccaatg aaagtgtccc aatcccccca gagtgagcta ccccgaacga 300 aaaagaagag ttagagcagc tacgtaaaga aaatcgtgtc ctcagagtcg tctcaagcga 360 gaagaactag ggcatcaagc ctacaagcta ctgtagagtt ggcagaagaa acctacggca 420 ttcagatacg aaaaaactcc gagccaagta gttcaccgtt tatcagagcc ggagcctagg 480 tatectattg tegactetge gaactgettg getttageeg teaggeettt tataaaegta 540 tctcaacgat ttagctaggc acgaggagga tgtcctatgc agtagtatat ccaatattgt 600 tggcacttaa gacaagcaga gcacctacct caagccgctt ccgagagctc atggtgcttt 660 gtcagcaata cttcggcccc aagttccgct tgggcgcgat cgcttttgcg ccctactcag 720 acgccatggt atgatetgcg caaacggtet gtgcgccete ggacaaccaa eteteggcat 780 aggectacaa gtatgaagac etgeteaata cagageetaa gtttgtgeet caagacetgg 840 ggaacteett gtageagaea teacetaegt ggettaeeaa gagggtttge etatetetee 900 ctactgaccg atgectatag tegetgtate gagggtattg ettacateeg accetggaag 960 ttgaaggetg tttgaatget tgeatcaage etttgettte ttaeggatea acatcaaatt 1020 gatacgacca tatgattcat catagegace gaggeattca gtatgeeggt aagagttaae 1080 cgatctgttg catgggcgag gctggcgcat cagtatgact cagacggaga tcctctgcat 1140 aatgcattgg ccgagcggat gaacaatacg ctcaagactc atggcacatc tcctcttcga 1200 aacaatcttt tgatcaagca ctecttetgt agaccgagee gtgegeatgt acaacgagge 1260 gcgtccacat caagtctaag ggcgaaaacg cctatgcaag tcattacacc ggagtctgaa 1320 aatcgttact ggcaaggatc gaacattgg 1349

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION $1...6\overline{33}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

gaaaacgaca	ttcttgacca	tgagtccgga	cgggcgagca	tecetacege	tacgatacag	60
gggcgtttgg	ttttagttaa	ctttttgatg	aaatgagcta	ggcagctgtg	aattgggcta	120
Lgctgatagg a	atttaatccc	tcatcggcat	accgcctatc	gtgcctcgta	tgccggagat	180
tgatttgatc a	aacgtctgat	attgtgtgat	gttagatgaa	tagattecta	agattagagg	240
tegggggggt (cagtcccgaa	atacgtattc	cacttccttg	taatatccgg	tcagectege	300
gaatagagcg a	attccgggcc	gattcggaaa	ggtacgatca	ggccacgcga	gctttattgc	360
caagcatggt d	catggggaaa	gcgactcctt	cgagacgaac	atatccaggt	tggaaccggt	420

cgtacatttg atcagttcga atgaatatcc ccatcgttgt acttatatat atagcggaat 480 acgctctcct aaaaccgcct gaagtgagac tgttgaagac atagatggag tccctctcag 540 attgaacatg aaaccttcca tcctgacgtt gatcttggtc ttgttcagac gggaggctct 600 ttccccttat ccagtacctg catataaaga tcg 633

- (2) INFORMATION FOR SEQ ID NO:23
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 713 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...713
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

60 ggcagtagee tgtteggeag cancegtgge etcaegateg egeaggttte caccatacee 120 tegtattega gtgetnecae aegattggee agetetatte gegtaeetta teegttgtae 180 ctgctccgat gctatccaaa tacctttgct ctggagctct gctcttcggc ggtcgttctg 240 catggetttg accttggttc gegtegettg gegttgagtt ctccgcggag ttgtacttcc 300 tgccgtgcag ttgggtctgc ttcatccgca gttcgtcctg caatttctcg aactcgtgcg 360 cacggactgc aagtccagtt ccaacaaggg ttcacctcgg tgtccgaatc gcctgcatgc 420 ttgagcacag ctatcagacg cgcctgcacc gggaagtgat gatctcctcg aaagccggca 480 ccacttegee ggaageegag gagegatetg cactteteet ttgtecacee geeceaaaeg 540 cagagagget eggatatgga geettggatg gaggagagea accaccatee geetaagaaa 600 gaaggactgc cgaagctgtt atgattgagg taaccgtctt tgcttttccg ttgagccgtt 660 cggcgaaact tgtctgtcat gaatcggttt cttttttcgg tgcgagcctt tgttgctcgc 713 cggcttccga agagcaaatg ccatgcaaac aaatccctgg ccttattaat cag

- (2) INFORMATION FOR SEQ ID NO:24
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

ggcgaagatg	taaccctgca	ggtatttgcc	ggtacggagg	ggattcccac	gatgccgaag	60
taatcttcat	gggcaaggct	ccctcgctca	aagtgggaat	cagttggccg	gccgtttctt	120
caacgcttat						180
ggcggtccgt	ccgttatccg	gtccgtcgta	agcagccttc	agagctgatc	gctaccggta	240
tegeegtate	gacctgaaca	atactttggt	gacgggacag	aagattcctt	tcttgg	296

(2) INFORMATION FOR SEQ ID NO:25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1207
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

ggcatgaatc	agttcaagga	tatcatactc	ggaaataccg	aggctaaatc	actcgtgtag	60
cagactcgca	gaagtgtttg	cgtgtaagcg	gcaagcacac	gacctcgaag	aggtaggcca	120
tgacacctat	catcatacca	tgttcgaatg	ctcggcaact	ggtcgttcgg	cgattacttc	180
aagaaagaag	ccatcgatgg	gcttgggaat	acttggtgac	ggtgttgggt	ctggatcccc	240
agcgttctat	gctaccgtat	tcgaaggcaa	ccccgaagaa	ggccttgacc	gcgaaacgaa	300
geggeatett	actgggcaca	gtttctgcct	gaagaacgaa	tcacaacggc	aataagcatg	360
acaacttctg	ggaaatgggc	gataccggtc	ccgcggtccc	tgctcggaaa	tacatatcga	420
cctgcgttcg	gacgaagagc	ggcccaaata	aacggtttgg	agctgatcaa	taagagccat	480
ccgcaggtca	tgagatatgg	aacctcgtct	tcatgcaata	caatcggaaa	gccgatgctc	540
			tacgggcatg			600
			acggatgctt			660
			ggattctacc			720
			gccatcacgg			780
gccaagccgg	ctatgtcatt	cgccgtatcc	tgcgccgtgc	ggttcgctac	ggcacacctt	840
cctacactgc	cgcgaagcgt	tcatgtaccg	attgctgccg	acctgatcga	tacgatgggc	900
gatgcttatc	ccgaattgca	agcacagcgc	gactgatcag	ccgcgtgatc	aaagaagagg	960
aagagagttt	cctgcgtaca	tggaaacggg	tatecgeetg	ctggagaaaa	aaatagccga	1020
caataaggca	ccggctccac	cgtattggac	ggtgtcgctg	ccttcgaatt	atacgatagt	1080
teggatttee	cctcgacctc	acagecetga	tcctatcgga	aaatgggtga	cggtggacga	1140
atcaggette	gacacggaga	tgcagaagca	aaaagacgtg	cccgtaatgc	cgctgccgta	1200
gaagccg						1207

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1845 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1845
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

```
60
tegettgaag cageaegeae ateategtag etgataeeea gttegtetae aagtetaeae
                                                                      120
teatetetet geteateete accaaatagt teagetgeta ttgegeggat tgegetgete
                                                                      180
cttgccatct atatagatct gattattctg atgctcaatt cttgtccggg catacccaca
                                                                      240
cagcgtttca catagtgtcg cgtctgtcca cggggcggta aacgatctcc ccgtagaaat
                                                                      300
ccggatactc caaagctcct cccgtcctac gagtttcttc cacatataat aatcggattg
                                                                      360
ggetgettga eggeeacegt ategeetgea gggaagttaa agacaccaaa tecceeteet
                                                                      420
tgacgtgtcc gaaaccette agtegettgt acgcaagaga ggtttgtccg agaacgattt
                                                                      480
gccacccgtc aatggcatcg tttgtgcgtc agcggcacac cgagcggagt cataggcgaa
                                                                      540
egeggteegt egaaagettg eteaegaaga ggtagtegee tataageaag gtetteteeg
                                                                      600
cgaagaagtc ggaatggcga agttctgaaa caggaaagcg aagataaagt aacggctacg
                                                                      660
acacagtaga taatgtctgc cacccagctg caaatgaccg aagcgtcttg tttcggatat
                                                                      720
tettatacca gececatttg ataataggaa gaaataataa tetaegatea aaggeagaaa
aatcagccaa aacggccggc ccatatacaa aaaaggaggt aaagaatagt aatggcaacg
                                                                      780
cetttatacg acgecatgge gteaaatett tecaatggaa ggteatateg ttatetgttg
                                                                      840
                                                                      900
ttataagetg attaaategt teategteag aaageetttg tggtggeage atatteggea
                                                                      960
gccaacacgg caccaagage gaatccetet caccaaaage ttegtggcat ategtcagee
gatecacete ggatgtatag atatgetgtg egtaceeggg aettegeett eteggatgga
                                                                     1020
                                                                     1080
ggtgatcgga gttcgttctc ctccggtgtc tccgtcagtc tccaagcgtc cagcgaggag
                                                                     1140
attoggotat caatocotog gocagtgtaa tagoogttoo gotoggaogt coaacttatg
                                                                     1200
tacatgatgg atttccgtca ggtgaggacg atactgtcgt gccggctcat caatcgggca
                                                                     1260
aacatacgac tgagcgagaa aaaaaattga ccccgatgct gaagttcgaa gcccagaaga
                                                                     1320
gggtetttee eteegtegge agegttette cageteggge agacgetetg tecacecegt
                                                                     1380
agtocgoaca coacoggoac ggaottatoo atacagogog agcaattogo atggoogoat
ccggacgggt aaattcgatg gctacatcgg ccgaacgaaa cctatcgaat cgaaacgatc
                                                                     1440
                                                                     1500
ttcctctccg gcatcgatcg tcagcaccac tcatgccctc ggctgcatgc aatccgttcg
                                                                     1560
atcacatgtc ccatcttgca taccctatca gtactatttt cataggattt tcttcttgga
aaaacgaacg tacccggccg caagggccaa aggtacacag atttagcgca agttcatccc
                                                                     1620
gtgatettge ggtacagate cagegegtat atateggtea tgeeggtata tagteeageg
                                                                     1680
                                                                     1740
tgcactgtat cttaccgtag aggetetect eccgttgttg tactgegtae ttaccegaet
gagcagcgtc cggctatagg catgtccgga ttggtgaggg cctgcatcat cttatctatc
                                                                     1800
agegeacega atactgatgt ceggeaaget ceacatecae caegt
                                                                     1845
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...573
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

gtcttggatg gt	gcggcgtc ggtatgcc	aa cgaacgctcc	acateggeae	cgtagcatcg	60
gccaagaggt ta	cccactcg ctcccaag	ta tagggggagc	gtgcaagtga	tcatagaaag	120
tcatattccg ga	agaattat ttcagatg	ag gaaagaggta	aacggcgagc	tggcttnggc	180
ttcggagcgg ac	gctgcgaa cttggctt	cg aaagccattc	ggccggcttn	cacggcaagg	240
cggaagccgt cg	ccatgctt acgggatc	tt ccgccacggn	tatggccgta	ttcacagaac	300
ggcatcagcc cc	catctcca tggcttct	gc cgcttggctg	ggccaccgat	acctgcatca	360
atgacgaccg gc	acacgact ctgttcga	tg atatacggat	catttcacgg	gtcttcagtc	420
cgcgattgct gcd	cgatggga gacccagt	gg catcaccgtg	gctgcgccgg	cttcttccag	480
atgcttgcac gca	acaggatc ggcctgaa	cg taagggagca	cgataaagcc	acgacgaaca	540
	cacgaage gtctcgat				573

- (2) INFORMATION FOR SEQ ID NO:28
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...464
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

ttagtggctg	aaatgcgatt	gccctgtgga	atatgcatcc	tgctatatcg	aaatgtgtta	60
tttttttatc	tttgtgcgga	ctttgttcag	agctgccttt	tcctattggg	atoggtggtg	120
atgattaaaa	gggaatcggg	tgaaaatccg	agcagtcccg	ctgctgtgaa	ccttqttaaq	180
ctttcggcat	ttatatcact	gtccgttctg	tgcggatggg	aaggagtogg	aaagtatggg	240
gtgaaccaga	agacctgcaa	agtctttgtc	tgcggcttcg	aggaaaagcc	gggaagaatg	300
cacttgtggt	caatccgact	ttactgccac	aaggatccgn	ttcttccctt	tcaatccccc	360
gaggaaaatt	ttgtttccga	cgcagcggaa	acatccgatt	cttttgctag	gaattggagt	420
gtatttgnga	gcggaccctt	aggtcttgtc	ttggcgggat	gage	- 33 3	464

- (2) INFORMATION FOR SEQ ID NO:29
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2759 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2759
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

60 tttttgggat tttggtttga gatttgggog attttcggtt cgagtttcgc ttgtgcgatt ggtgcctctg tttttttcga caccettctc tttcccttta ccctttattc cggaccaacc 120 180 gccaacattt cggtcaaaaa atctttttgt gcgagggaaa aaacatcttc tcatttcttt 240 tegtttgegg tettttaatt gttettaege gegegaacat attatate egeteeettt 300 tgtctctttc ttgggaggga gtccttttct tcggggggctg ttttttttgt cgaacggttg 360 aaaaaagatt ttgaaagatt tgtctgtaaa gaaaaaaggc gtattttgtg accgcaaaag cgattgctgc ccgattgata gaggaattgt tcgccgagcg cgtcgggatt ctttttttag 420 480 ggggaggate aggegaegag ettttettga gegteageee tgaaaaaaga geegattgat tttgccgatt ggaaaaaggt tttacttttg cacccactgt ccgctgcttg atcggctctt 540 gccgtgaggt gggaggatag gggataaaaa gacagcgatc attgacatgt tcatacgaag 600 aacaaaagtg tagtacaaga aggagagaga agggettgee atttettgea ggatttetge 660 cctctcgcag agaggaggc cgatttccgg ctgttattga cgaaaccgtc tctcgacgag 720 780 gacatatact ctgtcaagag aaaaacgaaa agaccgagag agaaaaagaa accgaggtgt 840 actactgata aatcgaatta tccaaagggt aataatcggc gtctgagcga gaaaacagaa gcaaacaaac acaaatatga cagtggagag tttgatcctg gccaggatga acgctagcga 900 960 taggettaae acatgeaagt egaggggeag etgatettag ettgetaagg ttgatggega ccggcgcacg ggtgcgtaac cgtatgcaac ttgccttaca gagggggata acccgttgaa 1020 1080 agacggacta aaccgcatac acttgtatta ttgcatgata ttacaaggaa atatttatgc 1140 tgtaagatag geatgegtee cattagettg ttggtgaggt aaeggetaee aaggegaega 1200 tgggtagggg aactgagagg tttatccccc acactgtact gagacacgga ccagactcct 1260 acgggaggca gcagtgagga atattgtcaa tgggcgagag cctgaaccag ccaagtcgcg tgaaggaaga cagtotaagg attgtaaact tottttatac gggaataacg ggcgatacga 1320 gtatgcattg aatgtaccgt aagaataagc atcggctaac tccgtgccag caccgcggta 1380 atacggagga tgcgagcgtt atccggattt attgggttta agggtgcgta ggttgttcgg 1440 1500 taagtcagcg gtgaaacctg agcgctcaac ttcagcctgc cgttgaaact gccgggcttg 1560 agttcagtgg cggcaggcga attcgtggtg tagcggtgaa atgcatagat atcacgagga 1620 actocgatge gaaggeaget tgecatactg egactgacae tgaagcaega aggegtggta tcaaacagga ttagataccc tggtagtcca cgcagtaaac gatgatacta ggagtttgcg 1680 1740 atataccgtc aagettecac agegaaageg ttaagaatee acetggggga gtaegeegge 1800 aacggtgaaa ctcaaaggaa ttgagggggc ccgcacaagc ggaggaacat gtggtttaat 1860 tegatgatae gegggaacet taccegggat tgaaatgtag atgaeggatg gtgaaaaceg 1920 tetecetteg gggettetat gtaggtgetg catggttgte gteagetegt gegtgaggtg 1980 teggettaag tgecataaeg agegeaaeee acateggtag tactaaeagt tttegetgag gactotaccg agactgccgt cgtaaggcgg aggaaggtgt ggatgacgtc aaatcagcac 2040 2100 ggcccttaca tccggggcac acacgtgtta caatgggagg gacaaagggc agctaccggg cgaccggtgc gaatctctaa accettcece agtteggate ggagtetgea actegateeg 2160 tgaagetgga ttegetagta ategegeate agecatggeg eggtgataeg tteeegggee 2220 2280 ttgtacacac cgcccgtcaa gccatgggag tcggggtacc tgaagggcgt aaccgcaagg 2340 ggcgcactag ggtaataccg gtgctggggc taagtcgtaa caaggtagcc gtaccggaag gtgcggctgg aaacctcctt tetggagtte ggaccgattg acataaacgg ttgcccgaaa 2400 2460 attaaggaga attggttgaa ggtagggttt tttgcaacgg aaccggtgtc gagatttatc 2520 cgatcggggg aagaagaaa gaccatatat cgccttcggt tcggctctcg gctttttttt tatccgaaaa actttactgc acggcgaaag ccatatttgt tcgacgtatg aataaaacga 2580 atataacctg cggatatccg atgcaatcaa gcgggatgtc cgggagggtg ttctctctct 2640

cttgaacgaa gatggagaga tacaggaaga taaggagtet tteeeteee egaggettgg 2700 ttegtttate tttegagett teeetgette gaactttget tettttttgg aagegagge 2759

- (2) INFORMATION FOR SEQ ID NO:30
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 558 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...558
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

cacagatgga gaaaatagcc gaccatatca gcgaatggga acggagggat cqqtaqqata 60 caacctacct cactoggaga cogtattgct gatgtacata acctatatgc cgatacgcag 120 atgaggggaa cgcgcttgtc ggcattctac aggatcgatt caacttcagc atgggaggag 180 gtacattttc tctcatccgg gtatcagagc ttcgtggtgg agcttcaaca aggagttgct 240 cgtcacccac gtatcagcgt gggttattct cccgaaagca acccggcttt ggtatgcgtg 300 cagccgccgg actttattat caggcaccgt tttacaaaga gctaggcaga cgcataagga 360 tgccgaaggc aataacgtgg ttgtcctcaa cggaagatcc gctctcaggg agcttttcac 420 attotogoag gagoagacta toottogaaa tggggggggg aaaatcaagt ttaoggoaga 480 ggcttactac agagcctgtt caacatcaac ccgtatataa tagagaacgt gaagatccgt 540 atctgggcga aaacatcg 558

- (2) INFORMATION FOR SEQ ID NO:31
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 655 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...655
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

gtagtttgaa	gggcagctga	ttgaactttt	cgtcatgggt	gtggaaggta	cggcagcctt	60
					gctgatgatc	120
				ctctccggcc		. 180
				gtatccgctg		240
				gatctcaagt		300
				ctgtccataa		360
				tctatgccga		420
				gctgaccgat		480
				ctgaaattcg		540
				tggaatacac		600
				catgacagtc		655

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...652
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

aaggcaacgt ggttga	ctgt atcgaatgcg	gttcgtgcag	cttcacctgc	cggccaaccg	60
tectetgetg gattata					120
aagcaataag aaagga					180
tccacagcgg agacag					240
cttggcatgt cggtate					300
ttaactggtn gcatcg					360
tcatggacgg ctcagc					420
gcccgtttgg atcatt					480
ggcggcttgg gaacaa					540
tttccctgcc cagatga					600
gagaccggtg ctacgc					652

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 714 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...714
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

ggttgtccgt	aaacgtggaa	ccgtgtctgg	cacgtgtatt	ggtcgtagga	aaccgacaat	60
	gagtacacay	yeyatette	CEGCTAtgca	++ <a+ <a="" <a+=""> <a> <a> <a> <a> <a> <a> <a> <a> <a></a+>		
atatacccct	tgcgccattt	aacaaaatat		cegacycage	tatggagaca	120
attogoctet		ggccaaatct	ccagtggcac	taatgaagcc	tatggagaca	180
	egeegaegee	acyccicaag	LEGGGGAGAG	daatogatag	~~~~~~~	240
agcatcaaca	acgtctatqq	gtatgtcaag	dcadacatot	++~~~~	tgtgcagcaa	
ccaagatgca	ngagagaga	9000000	geagacatgt	LLYacaatcc	tgtgcagcaa	300
ataaaa====	t	acggacttca	atctgaacca	agtgcgatct	atacaaaaga	360
	uaccctaaaa	actactttac	ggttatgtgc	cdadadtadt	a++ ~~ ~+	
aaatacgttc	ctcatggcat	cccggcgtga	adccada+42	22244046	ceegegegea	420
gtagaaggat	agtatagaga		ageeggatga	aggerggate	gaatttcagg	480
Jgaaagac	ageceggage	ayttcaaaaa	atacqtagac	aatcccattt	atacamete.	540
J J J C C G	acagoaccaa	yaayycgaaa	gctgacaatt	cattaataat		
togtoagtoa	tggaatacag	ntctattage	22+22	- Li	acaggiggal	600
ccatttooga	+~~	ntctattaca	aaccycaatt	tattatgcca	ttcctattcg	660
ccaccicega	ryaryaaaaa	gctnctacaa	agattcctac	ggcgtttcgg	ctca	714

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

acqaactqaa	aagcgtttta	ctassana	+ - + - +			
222222		Ccgaaagacc	tetatgacaa	tggcgagaaa	tcattcgaaa	60
ccaycagngg	cagatcgatt	cgctccqaaa	tgtattaact	tctacaacca	tttctcttcg	
atggagagtg	agatageces	20200		cecacaaccy	citetetteg	120
	agacageeea	agagetgaag	tgattttccc	ctctatcaat	teggetatge	180
rggtaccttc	gtccgggtqq	cacagggtag	ggattccgtt	ttaataataa	tggtgcgtcc	
gaaagccgga	taagggagte	~~~	jaccegee	cegetegteg	rggrgegree	240
Janageogga	caagecagee	ggaaataaac	aagctaagca	catggatggc	tacggtacca	300
agaccaagaa	agtgcgcctt	atcatagaca	ataatcatag	atagaaaa	aaacagtaat	
gcaaatgaaa	ttaanaarta	**	acaaccacag	gracaaccat	aaacagtaat	360
Janua	ccaaaaayta	rrettetegg	agagecetae	tattaaataa	++	420
gccaaagccg	acaaaggcat	gggctcctca	accentant	***	- caaggggca	420
tacatasast	~~~+++	333000000	acgaactcaa	ccaggagaat	ctggatcgaa	480
5 5-5-900	ggetttaeet	cccgtggatt	cgctctacag	tttcgacaag	ccatccatac	540
atgcccgtg			,		cegeceatge	540
						549

(2) INFORMATION FOR SEQ ID NO:35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

 (ii) MOLECULE TYPE: DNA (genomic)

 (iii) HYPOTHETICAL: NO

 (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...687
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

60 aggtcggtaa tgatgcgatg tgagtggcat agacagtggc ggcaacttct caatagcctc 120 tatgtccacc ttttcgagca gtttgcggta gtactgctca tgccatggat tgtctccgag agagetgaga agtttteggt gtegegagga gegegagtgt gatettgegt ttgagteeet 180 240 ctttcttqtc ccqqctatqc tccttqaacc atctqcacaq aacqtaatac cqaqqaaact gaaaggettt ttatgetega taccacaaag teeetattea getteageee tttgggtatt 300 tcaaatgttc gctcaggtct tggagagcat ttagcggatc tacttctccg gcaagaagag 360 tagcaggtcg tcggcatagc ggataaattc ggtgttatat gcccggcgat gtagcgatcc 420 gtgtcttcca agtagaggtt gaaagcagag gggccagagg gcttccctgt gggatgccgg 480 540 aggatgcacg gcatattgct gcttccggtc cacgactccg gacttcatcc agaggctcac 600 atacqqqtaa qqaaqqqatc ttcqqttqtt ctttqqactt tctqcaatqa qaqqqqacaq ggatagaatc gaagaagttg tcaatatcgc agcgcacact gtatggttct catccagaga 660 687 atccaqcaga tgctgcactc tacgaag

- (2) INFORMATION FOR SEQ ID NO:36
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...300
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

gagttctgct	tttttagctg	aatccaaata	cattttcttc	cgttttttac	gtgttaaaca	60
			ctggccgcaa			120
cacagegega	atctgtttct	tegetetgtt	ataacgatgc	cgttggacgt	acggatctac	180
attgggccaa	gcattcagga	aaggtgaact	cgcccttctt	tgcatttttg	ggtccaaaaa	240

caagcaagaa agccgagatt ctatttactt ttgtgcactc tttgaacgaa aatncgctta 300

- (2) INFORMATION FOR SEQ ID NO:37
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 746 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...746
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

gaagcaaaat ttgtcactgc angcatgtaa cagtattttc tgcaaccgaa tcaccgtctg 60 caaacttgaa tcaaagagat actaatcata agcaattatt tctcaataaa ataatcatta 120 cttccatatt tagtcatagc tatcatggta cttatttcaa attcctcagc cgcaacaaac 180 totacacctt cgttacatcg taggetttge ectetegete atattegtet tgetgettag 240 cttcttgtac ggcgcgaaca gcaagccgat cgtattcata ccgattacaa acgttctatc 300 agtacaatgt cgagagtaag aataactgga gcggatttat ctgtgctatc ctgccggaac 360 gctcattcgc gagcaggtac ccgatgtgga aggatatgcc gcatcagcga atacaacgac 420 aaggaataca tetttategg teegacaage aaaaegggtt gattgeetee catetttegg 480 tegaateeaa ttetttaett tettegaegg etataaaete ettgagggtg ateecaaaat 540 gtcctttccg agcagaacag tgccgttatt tcctccgcgt tggcagccgt atcttcggta 600 acgtgtctcc catcgggcag gagatttcgt ttttcgattt tccaaaaaca agcagacctt 660 teggateaeg ggeateatgg ageegageeg gataaetgee atateagaee ggeegaaete 720 cttttctatc aggagccaaa gaaaac 746

- (2) INFORMATION FOR SEQ ID NO:38
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

```
ccgnttcgca ggaatcgaag gtgatgatgt cggtgtagta gtcatgatca gaaattcctg
                                                                        60
attgqctttc agnatatatt cgtcatcaca qaaaaqatgg agatttctcc caccgctttc
                                                                       120
                                                                      180
ccatatogge tgcatactte ggctatcact taccgacgat ccgtcttctg atccgaggaa
ggctgacgcc ttcagctaga aattgatttt tgccattgtc ttaattatcg ttttgctcgg
                                                                      240
tcacctaccc tcaaccaaag aaaatataag tgacagcaat ggctgtcagc gctcggccaa
                                                                      300
atcggccaaa agggaatagc tcaccgtata acgtgtattg cgtttttgac ggctccatag
                                                                      360
                                                                      420
tagagggeta egacgtagaa egtggtateg etgageeetg tacaataetg catagaegge
                                                                      480
egacaaaget gteggeteeg tegtetgeat ggeategace atgageeete tggeteeact
                                                                      540
teegetaagt gitteattag eatggieggg atteetteea caaacticat ateteeteee
                                                                      600
aaaageegae cagteegege aageetteag tgateagate catggeaegg aagetetgaa
                                                                      660
tataccgata ccgaccagca tggccagcag atagggatga tggtcacagc cgtaccgaaa
                                                                      720
ccatcttttg ccccttcgat aaaggctcat acacattgat gcgtgcacgc agtccactaa
tgacgaatcc gcacatattc caaacagaag aatggatgca aatgcagtgc tgatacaact
                                                                      780
                                                                      840
aaattttccq qaqqcaqaqt ccqtcctqca taqattaccc ctccqataaa qaqaqaqqq
                                                                      900
aaagaaqaaa aagaaqaaga ggtttttgga agaaatcgat acctgcttga tccctactgc
                                                                      960
aaggatggcg accaatgtgg aagcaaacgt gcaatcagaa ccgggacaaa gatgtcggta
ggatttgccg ccccgacctg aggcgatagg ccatgatgga agagggaatc agcgtaagtc
                                                                     1020
cactggcatg atggccaaga acataatcat ggcatcgctg gctttatctt tttgctgatg
                                                                     1080
atogtttgca aactotocat ogaacggata cogagggggg tagcagettg tcaaggcota
                                                                     1140
acaggttggc cgatatattc atgaagatat tgcccatgcg ggatggtcct taggtacaga
                                                                     1200
agggaacaat cggcttagaa caggtaactg atctgtgcca gcttgcttat aaggccactt
                                                                     1260
cgttctgcta ttttatcaga ccgagccaca gagcgagtac actggtcagt gcaagggcta
                                                                     1320
                                                                     1380
totaaaggoa ttottogact ggotgaaaga agootgoaco atogoatoga atoggacaca
                                                                     1395
tcgccgaaag ctatc
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 531 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...531
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

gtgtgctgcc	agagcctgat	cgccgagtcg	cccgacaaaa	aggacggcgt	ggtgaaagag	60
gccgattcga	gtcccatctg	gacggcaacg	gggagtccac	ggagaatagg	cggcggtagg	120
cgcgacggat	atgcatctgc	cggcagaggc	gtggcggatc	gctgtccatg	agggtctgcg	180
atagaggaaa	aggacgtggt	gacgagcatc	agcaggcggc	tcaacagggt	ggcatagccc	240
gcaccaggag	tcccatttcg	gggagaccgc	ctttgccgaa	tatcagcagg	tagtcagccc	300
gacattgaag	agattgcccg	atatggtaat	atacatcggg	gtggcgtatc	gctcatgccg	360
tcatagaatt	gcttgaaggc	attgaatacc	gtacgaggaa	gaggcctccc	acctgtaccc	420
aataataggg	gatggcgaga	ggcggagcga	gggtgggagg	ttgaatgtat	cgaacagggg	480
aaccatcacg	ctgccacacc	tgcgaggaag	agtccgatcg	ctntattgag	g	531

- (2) INFORMATION FOR SEQ ID NO:40
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 647 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...647
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

ggctctaacc cgaatacgat ccggagacca atagacaatc cacaagacta acaacgaaag 60 gagtgegteg atcegaaaga teeggegeae tetttgtaag atteagattt gacteataaa 120 caatcaatca gcggacttca ttctcttaaa taagtatatt cgcaaaataa ataagctgat 180 tacaagtaaa atcaacttat cttaggttaa agctcaaggt aaattgagta tactctgggt 240 taggagataa ctatttagtt aaagaaaata agaaaaaact tattcacgct aaaaatggca 300 aaaaaattca aaatagaacc tattaacaaa aggcatatga cacacacgaa gcaatggaga 360 aattactcag agaggctgga agaggtatga caaagataaa atcgcagaaa aattaattaa 420 480 gcaagcacat cccagagatc ttccatcgca aaggcggaaa aatttctcta gttaatagaa 540 tagaacacaa caatceteat caaaagaagt atcaaaaget eetaaaaaac aaagcagate 600 cacagaaaaa atatancata gttgaaaaga gctgctaacc aactaaa 647

33

- (2) INFORMATION FOR SEQ ID NO:41
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 606 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...606
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

ggcgaaagcc tgaccgattt cctttttgcc aagatggggc tgaacaaggc agtatcgcca cggctgtgga caaactgata gagaaactgc cccatgtacg ggtggcgaac cctatctgtc

60

120

gcatgagacc	aatcaggtgc	tacaggcgcg	gaggacgcag	cgcaccggat	gaaggacaaa	180
tacgtctctt	tagaaccatc	gtgctggcta	ttctgactac	gcgatgcgag	gcgtccactc	240
tactcaggat	accadaacca	ccgaacagct	tctgcagtcg	gccatcgaag	agctcggaag	. 300
adacacaaca	tgaccagtca	gagtgcggag	gaacagtaca	atgactggag	aaatatgccg	360
tcaatctctd	tcagcgtgct	cacaataaca	agtggatccc	gtgatcggtc	gcgatgacga	420
gatcaggcga	atactacaaa	tetetetega	cgcaccaaga	acaatcctat	ccttatcggt	480
gaccaggega	dacasascaa	ccatageega	agacttagct	tacaggatcg	tacataacac	540
atacagaga	atatacacaa	caadcadata	ttctctctca	acatgggtcc	ttgatcgccg	600
	accegegeau	caagcagaca	ccccccc	,,,,,		606
gagcca						• • •

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...999
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

aggtgtggaa	gtcgcaggat	ctgaatatct	ttcagattat	ccagcgcaaa	gcaagggact	60
aattatatat	atcaacaaqt	gggacttggt	ggaagataaa	gtcaagccgt	catcaagacg	120
tttgagaatg	ccatccggca	gcgttttctc	catttacgga	tttccctctt	ctcttcatat	180
caactataac	caaacaaqqa	ttttcaaagt	gttggagacg	gtcaatcagg	tctatgcaca	240
ccactaactc	gtattcccac	acacaagctg	aatgaagtga	tgctacccat	tatcaggcta	300
caccaccacc	toctaccaaa	ggtaaataca	tcaagataaa	atagtgatgc	agcttccgac	360
agcagtgcct	tcatttqcct	tttttqccaa	tegeeteagt	gggtgaaaga	gccttataag	420
cattttttaa	agaatcagat	tgtgcccact	qqqatttttg	cggtactccc	atcaacattt	480
ttatccgcga	aagtagggtt	tgcccctqct	caatacgttt	aagtcatcat	agaagaataa	540
atgatatgga	atggaaacgt	tttagatttc	tgaacaatgt	cgtcggttgg	gcgtttttgc	600
agttgcagct	atcatctatc	tgatgacaat	cgagcctcag	ccagcctgtg	ggactgtgcc	660
gagttcatag	tctgcgtaaa	caaqttqaqa	toggtcatco	gcccggagca	cccttcttca	720
tactcatcta	taatacatat	cgcatttcac	gagcgatccg	tcacaggtgg	catggcttgc	780
caatctacca	gtgcactggc	cagtgccttt	accatectgt	ttttgttttg	gacattaccc	840
accttqtccq	ccqcqtactt	gtaccgacag	tacgcaatgt	atcggattgg	aagagccgtc	900
aaggaaaata	tectttecac	gagtaatcac	gtactcggca	gtggagtcgt	tggagccttg	960
	tcagcgatac					999
-						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1241
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

ggtagaggaa agcctgaaga ataagtcttt gacgttttgc acattggctt ttcttccagc 60 atgtgatcgt cggggttggc ccatgccacg aaagacacgt agtggggccg tcgtattcca 120 atggtategg tttgegtgea geeactttge ggegteeate ateagteggt egatgeggeg 180 geeggttteg tegaaaegaa aataaegaeg egetgeaegg eteeggttte ggtaatatet 240 300 tgcattcggc atcccaagcc ctgacggtca ggcgaaacgg acggggacaa tcggatagtc 360 ctctttgata catccgccaa acattccggc cacgagtaag atcgcaccga tacgatatat 420 ttcttagcgt cgttcataac aataattctt tgttggtgat tgggatttcc ctatttgatt 480 tggaqagaat gaatacaggg atggagcgaa ccccgctccc tgtattccga tatagacaaa 540 ctatgaaagt ttttagtcgt ttgacgggtc gattaccaag tagcagcctg attaacaaca cccaaggtgt aacttggcaa gtaacattca ngttggcttg taccggttag gattttcaag 600 660 gagtattcgt accgggcccg gtgatgttca gcgaaatttg tantgggttg ttgcgaacga 720 ttttgttttg tccttgggta atagcactga atagatgtag ccattgccat catagttcac 780 caataccgga tagtagtcgt gccatctccg tcgcagaatc cggcatttat agcatccgtc aaggtggttc cgtgagaggg ttgccgtcct tatcgagcag ctttccatag ataaaaggat 840 900 cgtcggacga agctcgttgc ttgcatcata tttactttcc agacatagaa acccggcacc tacagcataa ttcgtattca aagacgcctc cattcgtatg tttctcctgc agcatccgga 960 gtgtaaagac cggcaggcgt tggactccat acaaatatgc attagtgttt gagaccaaag 1020 1080 aattgccgaa atcttagaat ctttctttgc gacaagggct gcgattttag cgtcagctgt 1140 ttaaaagaat agtagttttg atactgtgta gccatattta cctctaccct gcgaatgaga 1200 taccggcatg cacccgagta acggcaagag gagttcagca gaaacaaggt tgtcggatgc 1241 agtcccacca ggatagccat agtggtggag cccggtttga t

35

- (2) INFORMATION FOR SEQ ID NO:44
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...627
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

geteatgeae caaacaatae aactetteae tetgettegg egtaagegae eeatategaa 120 ccacaacteg ctgacaggge cgtagecegt gaggatette tgacetgaeg catattgtat

60

tggtgatgtg	ccggagtaat	ccgatcacat	tgtgatcgct	gatcggattg	gcttccggga		180
aatgccaatc	aataaggaga	agtaaacgcc	gaacttcata	cccgaacgct	cacaagcatc		240
gctcattcct	tcatcacatc	gcgacgcgaa	ggagtggcct	ccactatatt	gaatgagtct	7%	300
cageegagee	atacatgcag	aagccatcgt	gatgcttgga	agtaacacga	tactcttcat		360
ccctgctttc	cgagctaagg	ctactatggc	atggcatccc	atctgtcggg	gcggaaccgc		420
ttggccaccg	gctcgtattg	ctcatgtcgc	gtattccgaa	agagtagatc	tgttcgctat		480
atccgttctt	actggtttgc	cttgccaaac	ccctccaagc	tcactgtaga	agccgtaata		540
atgaaaaggc	tgaatttgtc	acgatgccaa	cgctcgaagc	ttccgaattc	gttgagccac		600
gaggaataga	gacgagaaac	aaacggc					627

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 665 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...665
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

60 attacaagga aacctettga tegtaagegg ateggeagae gacaatgtta tetteagaae 120 acgatgettt ttacagagge actggttcag gecaatatee ettegacatg getatetata tggacaagaa ccatagtata taccggggga atacccgcta tcatctctat actcgcaaag 180 240 caaagttttt gttcgcatct tttantacag nttttctcag ttgcttgatg gggcgagtgg 300 cgaaggggtt tttgttcact tgctccgttc gacagtggtc tctaatagct ctttttgaaa 360 aaactatggc gcaacacgtc aagaaacccg aatggttgaa aatcgtcttg gtgggaatga 420 gaagtttacc gagactaaaa gcattgtcga ggacattgtc tgcatacgat ctgtacaagt 480 ggcaaatgcc ccaatatggg aagtgctgga gtagggggac tgctaccttc atgatcggtg 540 gtgatatetg acacgtgeet gtegattttg caacactttg acggggegte ccaaacegee aatgaagcag aacctactca cgtcgcattg agtatcaaac tgatggggtt aaccatgctg 600 660 tggtgacgag cgttgaccgc gatgacttgc ccgattaggt gccgcacact gggttaagac 665 cattc

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 604 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...604
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

ggatacggcg agctgccgag tggaattcgg cacggggcga cttcggcccg cctatgcacc 60 cgatgcttcg gctctctatt tcacatcgag cagaagcaag acgacggttt ggataatagc 120 agcataacgg gactgaaacc caacgacttt atatcatcaa acgagatgca caaggacgat 180 ggggacgtcc cgataggtgt ccggaggaat caacactcca tgggatgaag gcgtgccaac 240 gatcagcccg atggtagtac catatattat acgttggcgc agcaaggagc cgatacgacc 300 gtacggtaca gatctattcc gccgctcgga gcggagaagg cggtggagca acggttcgct 360 cgtggacatt atgcgcgatt cgctccgtat ggtgctcatc ccctctatgt cggcaatccg 420 gcgattacct gtatttcgtc acaatatagg cggtagctat ggcggcaagg atatttatcg 480 tgtcaaggtg cggatcgttc ttatggttca ccggagaatt tggggcctga tatcaatacc 540 cgggggacga aatgtttccc ttcatagatg ggggattagt acceptttct ttcgcttcgg 600 604 acgg

- (2) INFORMATION FOR SEQ ID NO:47
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 610 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...610
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

aaccatttaa	ctccaaactt	ccttgtcaag	aststtasta	agggatgttg	agtettteet	60
			-			00
ggtatagggg	acaagatgtg	cttttgctct	tcacgaacag	cctgactcca	ctaccgctac	120
atcattgaaa	gtatggagag	ataaagagga	aagacaaagc	cggaaaccct	tactctctcg	180
ctctttgcac	cggactatct	ctccgtaaac	tcatcaggaa	gttggctttg	cccggacgtg	240
tggcacggat	agtatcggac	aggtatcgac	acttctcgag	cgatatggca	tagaagcctt	300
ccatatacta	tccacatcga	cacagccgga	aatatccgta	gccccgtgca	agctacagtc	360
tccgatagtc	ctttcgcacc	ctgtttcttt	atatgttagt	aaagaccttt	gccgctgctc	420
tgcacagcat	agacgccctt	acgttaccgt	cgaagtcaat	atcacccgag	gttgctatct	480
caagtatggt	ggactccccg	atgcagcagt	ccgtgagagt	ctggatagga	ttcgctccaa	540
tacgactgtc	tgaatatcac	ctttcccaaa	agagcattac	gatcaaattc	agtccggcag	600
acattcaaaa						610

- (2) INFORMATION FOR SEQ ID NO:48
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 557 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...557
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

ggggacacgc	atcagtctgc	atagctcggc	agagaaggtt	tcacgcgtcg	gcgaatgccc	60
agcgatccgt	ccgaagcgat	gagtgccggc	gccacgcctt	ggcctgagga	tagatgatgg	120
tcagcggttt	ggtcgtcagc	tcgatcaatc	ccaggccaac	teeggeactt	cgtccatgag	180
gccttggagc	ttcgctccga	atcgatgaag	gaccaagcat	gctctngctg	teegetettt	240
ctttcgccgg	taaatccgct	ggacggcttc	ttcgttcgtg	gcatcgcagc	ctatccccaa	300
atggtatctg	tcgggtaaag	gatgattccg	cctttgcgca	tgattcggcg	gctttcttcg	360
cttcacttct	ctgaatatcg	ttgagcatat	cgtgggtata	tctctatttt	ttcgagagag	420
ccgagtgcgc	tcactccttc	agggcaaaag	tatgaatatc	tgccgtatca	atgctttaat	480
atgtcatttc	tagtcttcat	cggttatttc	tgtctgtttc	tttattttat	aaatgatcat	540
teeggeegga	gaaagtt					557

- (2) INFORMATION FOR SEQ ID NO:49
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1073 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{0}73$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

gcttcgacaa	ctcgaatata	cagggtacga	gtccggtggc	agcctgcgtg	ttttcaaaat	60
			gtttcacgga			120
gacttcgcct	ccatgagaga	aatcatcgtc	ggcattacac	ccgtctgacg	gaagagaact	180
tacccctacc	cgacctatcg	tcgtagatgg	agggaaagga	cagcttagcg	cagcgtacga	240
			atacccatca			300
gaggaaatct	ttttcccgaa	ggaccccgtt	ccgctgattt	tggcaagaaa	agcgaaacgc	360
tcaaggtcat	acaacaccta	cgcgacgaag	caaccgcttc	gggatcgggt	tccaccgcga	420
tgtacgaagt						480

acaaaagaag	tetgeteege	catttcaaaa	gcgtaaagcg	aatacgctcc	gcagaagaga	540
	gctcttatcg					600
	cgatgagagt					. 660
	cagccgtata					720
	gacatgaact					780
	gatgaacctt					840
	atgggatcga					900
	gccatccctc					960
	gacaaggcgt					1020
	ttgattgaca					1073

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 839 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...839
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

```
60
ggcaaagcgt tccaagaaac cgatggcaac agccggtttg ttcattttct atagatgcac
cggctttcgc attgcttctc ttgcggacag acacgtccca caccgccggc aaagagcttg
                                                                       120
tototogoaa agtagatgot goagocatat atogootact totatotgot tgataaaggt
                                                                       180
                                                                       240
cgggatattg atactccagg acatccttcc atacagctcg gttgcggaca atcgagacaa
                                                                       300
cgagagette ggeeatageg geeteaeggg acaaacegeg atteaeetet teatgatett
                                                                       360
ggagctacga tagagggggt cgagttcggg catttcagcc cgtgacgcga catgcgttct
                                                                       420
ttatttttga gegegttgeg eageteetet eteatggtte agagegaege agteggataa
                                                                       480
gttcttctgt agtcatgtca aaaggcagaa aataaggtta ttccatctct cggtatgcgc
                                                                       540
ccaaacgcat atcatctcat cgaaatccac ttggtgtgca tcgaattcgg ggccatcgaa
                                                                       600
cagacgaatt togtotgtoc toccacgott atacgacaag coccacacta coggtgocat
                                                                       660
ccaccataat tgtattgaga gaagctatgg tcggtattcg taacgtttgg tcaggagaga
                                                                       720
aacgaactte atcateacag eeggeegate gtaacgeaga ggtetacegt tteeegtttg
                                                                       780
ataacgettt ccactcatce gttacgagge etttegtece ataagaccea tegtetgtea
                                                                       839
tgatatcact tcatcgctat tggctcgcat tgttcttcag gataaccaga tctagttct
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 628 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...628
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

```
tataaaaaag aaaaaagagt ttatggggat accgattatg accgatttgc tttttcacca
                                                                       60
atcgtttttt acaatcattc aataaggcag ctttcgatac ttttttagct ccagagtaga
                                                                      120
atatccaaat caaatcaaaa tattattcaa atgtttttta ccaaaatgga gaaattaaaa
                                                                      180
actgacgtta ttgcattgcc cagatattgg gttagttggg ctcaaccaag ttgcatattt
                                                                      240
tgcagaaaag aagaagccga ttcatgaatc tctccaggaa atatctttga agaaaagcta
                                                                      300
aatttttagt gatgatggag agcagtattt atgcagcaaa gcgggagatg ctctcattgc
                                                                      360
tcaaatcctc attttagcag gaagattatc aagaatgaag ctccaaaaga ggcattgctt
                                                                      420
ttcatggaga agaccattac cgagaaatag atttgtctgt tgcaaagaat cttctaattg
                                                                      480
catacatgcg attctgcaga gaatgagaaa caacgagatt tgaacagcgt taaaaacgag
                                                                      540
acgeattace atetgatata aacattgatg aettaacana cacataatet teatatatgg
                                                                      600
aaacaaaaa attgcaggag ttttggta
                                                                      628
```

- (2) INFORMATION FOR SEQ ID NO:52
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 672 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...672
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

ggctgcaagt	atcgcgtccg	gatcagtgca	caacggtatg	gtttcattcc	atcgaatgct	60
			ttgggtggtc			120
tggcagaaag	caaactttcg	cccaacggct	gtcgcgtatc	ctctactccc	acaagcagat	180
gaatcagcag	ttcgacggaa	gcaaaaggaa	cgattactat	ccatacaggc	aaagctgttt	240
tectetacga	caaggaacaa	caacctgctt	atcgcacttt	cgagcagtat	atgcgtggga	300
aaacatccct	aagtatatgc	tcaacagcca	gcaatcatgg	cgatcttcgg	attagatacg	360
gtttgtatgc	ttctcgataa	ggaattgctt	gatttgccta	ctctcttccc	ttcgaatacc	420
gctacggaaa	gcgtatctat	gtgatatttg	tcgtgaactg	tatggcgaga	aaggcatttc	480
tttttcggac	atttgaacct	gcatggcatt	atctcttctc	ctgtttaccg	actcaaacgt	540
ctctaaagcc	tttgcttcga	ccatttatac	cccgtccttc	gatttggaag	gcgatattat	600
cggttttgga	acggatcatg	caacctgtat	taccgacggt	agagcaagga	cgacgtttcc	660
acccgacatc						672

(2) INFORMATION FOR 10 NO:53

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

cgagaccatt gcacaaatcc agctcaccaa taccgaacaa gtttccttgg tttttgagca tttagatgtg ttcttcacct tgaatattag tccccaggtg caaaacagac gagaatggtc 60 aaaaacacac cgggaacaag ctagcagaag aacagcctct ttgtgcaatg gtctctaaat 120 acgagtatag tccactaggt gcagagaaaa cctgtcgaaa gccggcttta gagagttatt 180 cattatetge aageagtact teggagagag gtttecateg gtegetattg gntgeegeea 240 gttaaaagcc ggcgacttaa tgccctgcaa tcggcgtttt cacctaagac aaccaatacc 300 tgatacaccg ggacaaccgg ctcaatatag agctgaacne tgtactcgga agtccacgaa 360 agtacacatc gctactccct cccccgtacg atggttcagg ctccaaaaat tgccggcttt 420 acagccatga agcgtggcgc gtaatttttt gcgttttggc tcgggaggta aaatttttag 480 cgccaaagcg aaaaaattct cgccccgttt tctcaggatt tacagaccca atccgagcat 540 tttcggctcg taatttatcg aagtgacaga ntttacccat taaagatgac gtgtactgaa 600 660

(2) INFORMATION FOR SEQ ID NO:54

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 641 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...641
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

gaggaaccag ctccttttgc ttgatgaacc aaacaaacat aatacgcgta ttaggcggat 60 tatcttcgtt tctagatctt ctctatcatc ttcacttgac tagtatcatt agggaaactg 120

atateggeet egggagatat	ggcccacggt	accactcgaa	gagatccttg	tagaactgtt	180
tegteagtge etegacgaga	aagcatcctc	aatatctttg	agttcgatgt	cttggcgttg	240
tttctgtcga ttaacttctg	gaagttqtct	gctgctgtac	caaacatgtg	ttgccagggc	300
cgagcaagaa ggtgaaacgc	ttactactaa	taatgtogga	ctgctcctcc	ccttgtggca	360
gaaggtaaac cgccattccc	acaaaggatt	gtctcgtagt	ggaatatcat	aaaagcactc	420
gaataggtgt catgatacgc	cgataatatt	ctggatgcca	accttattqc	gagccatctt	480
gatctggcta ataccgtgat					540
cgatatgctg atctctagga	tacccattac	ttatactact	agtcatagtc	gggtacatct	600
				333	641
ctaggataga tcaccatgac	Catectcaaa	caycoccacc	u		

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 674 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...674
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

```
gegeaggatg tagecetttt eteegetete atgaacegee ggaeggatgg aegeeacegt
                                                                        60
toggooggtt attttatoto aacottaaco atogtotoca tgaaatgtat cattgoogag
                                                                       120
                                                                       180
aaaccctcgg tcgcccgcga catagccgca tcgtcggtgc aacgcacaaa gaagagggct
                                                                       240
gtttctccgg aaacggcatg tggttacctg ggccttcgga cacctcgtta cccttgcgat
geoegageat aeggetttee gaegtaeage egegageaae tgeeeattat eeceaacett
                                                                       300
teeggttagt egteegacag ateegeaaag gaacgaeeta taegaegaee egteegeett
                                                                       360
                                                                       420
gaagcaactc aatatcatcc gcaagtgttt cgccgaagcg atcacatcat cgtcgccacc
                                                                       480
gacgccggac gcgaaggcga gtgatcttcc gcctgatcta tgcttatttg gattgccgca
                                                                       540
aacetttega egeetgtgga teageteeet eacegataag getateeegt gagggaetge
ccgtccggct gacggccggc agtacgaccg cctttatctc tcgggcaagc tcgcagtgaa
                                                                       600
                                                                       660
gccgacttgg cttgtcggta tcaatgccag ccgggcctct catcgctcgc ggaggcgctt
                                                                       674
attcctggga agag
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1930 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1930
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

gcctatetet gtgatgacaa agteggtaet gactettttg teccaggagt tgaegttgeg 60 cttgatctca tccgtaatat gaggcaccac ttgcacggct tgcccaagta ctcgcccttg 120 cgttccttgc ggattacgtt ctgatagtcc tgcctgtcgt gatattattg gcacgagtag 180 tgggcgtatt gaggaacgct catagtggcc gagatccaaa tcggcctcat gtccgtcctc 240 ggtgaatagc attcgccgtg ctcataagga ttgagcgtac cgggatcgat attgtatagg 300 ggtcgaactt ctgaagagct acgttgaaac cgcgagcttg gagagtttgc cgagagatgc 360 tgctacgatg ccttttccaa gagaagaaac caaccaccgg tcacgaagat atacttagta 420 tctgccatag cgcgaaaaga tgtattgttg atactttgat cgataaatca ggggtacgga 480 aagctacccc aacggaccag cetectecga ttegtgegea aatatacaaa aagaaegeeg 540 ctaaaagagg caaatacgac agctcttgcc cgatgccggc acatcaaatg agaaatgagg 600 catccgacga accgcgataa ggctatccga ggcaaattac gcgccggaaa tgctccgatt 660 geggttegta aattetegaa aacaeggega gatttttee gttttggtte gggaaacaaa 720 aaatttacgc gccaagcgaa aattttctcg cgccacgttt ttacgaacga caatggagcc 780 gatttggaac cgagacggca atatgagcag catgccccac gagtcgtttt ttctctcgca 840 ggataaggta tttccttagc tggataagaa ggaaatgaca ccaccgattc atagcaaaaa 900 gcatggtttt cattccgaca acaaggtgtc aatgatgagg gcaaactcga tcgtaatgct 960 geoggeacgt tgttegaate geacetgega teaaagattg getgtttggg aaaaaqeata 1020 taaatttgga ggaaatttca gagtttcact cctaatacta catcagaaca tggctgtctc 1080 atcaatgaag tttccaggac gttcggcgaa tatcttctta ttcccggctc actacagaac 1140 agtgcactcc ccaaaacatc tctcttcaga ctcctccatt aagttcaatc gcgatgagag 1200 teccegtate aagetgaata tecegttgtt teggeeatea tgeagteggt etecaatgat 1260 acgetggeea tegattggea egeaaegggg gaetttegtt tatettegga tegeagagea 1320 taggagtcag gccgaaatgg ttcgtcgtgt aaagaaattc aaggccggat tttcaccagc 1380 gattccaatc tcagaccgga caatacgctg gccgatgtat tgatctggtc aaaaggacag 1440 gacataataa tataggtatc actcacgacg ttcgtccaat ggccgtctga tgggtatcgt 1500 cacgagcaga gactateget cageaeggae teaceetega ageeggteaa agattttatg 1560 acgccgttga gagacttacg gtgggcaagg tcggtattac gctgagcgaa gccaacgtat 1620 tatttgggaa aacaaactca atacgetgee gateategae gaaaatagaa tetgeagtat 1680 ttcgtcttcc gtaaagatta cgacagccac aagaaaatcc gctcgaactc tccaactaca 1740 cggacaagac cctcctcgtg ggtgcggtat caatacacgc gactataagg agcgagtacc 1800 tgcactggtg gagccggtgt ggatgtggtg tgcatcgact catcggacgg ctattccgac 1860 tgcagagcaa tacgatccgt tggatcaagg agaaatacgg ggacagtttg tcgtaagtgc 1920 acggaatgtg 1930

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

cgaggtagec etgetttgte tgtecaetea tteatateat tgagggaagt ceategaaga 60 taggtgtage aaatttgaca ttcatcttge gteeegeeag geaagtaceg ettegaatat 120 ctqtcccagq ttcatacqqq aqqqtaccca aqaqqqttta qqcatatqtc taccqqaqta 180 ccgtctgcga ggaacgcata tcctcttgac gcacgatttt ggacacaata cctttatttc 240 catgagteeg gecatettgt egecaacttg gatetteegt ttettggeta tataactttg 300 gccatttgaa caataccggc aggcagttcg tccccgatgg tctatctaat ttgcgacgcc 360 gtagttcage ttcaatctce ttggagtget tegataatte accgeaacag cettaatcaa 420 ctcgttcgta tgtgcatcat tgtccaatca cttaattgga tcacattgaa atcaagagct 480 teaagatett tttggegaat ttgetgeegg eettaateaa eteaacatte aagtagteet 540 tacgccacag caggttttgc ctttggtcaa gttctggtag cttgtcgaca gacgcttcat 600 gaagtggtgc tgccttttcg cgtatgtttc 630

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION $1...1\overline{119}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

gcaaactctg	aatgatccgt	ccgcacatag	caccgatgta	ggtacgtcgt	gtccacgaat	60
ctcagcttcg	tcatgcaagc	cccctaaaga	aatgcgtagt	atttacgacc	caagctctcg	120
gcaatgctct	tgccaagaga	ggtcttacca	ctcccggagg	gccgtacaga	cagatgatgg	180
gcgacttcat	atcgccttca	tcttgaggac	agccagatgc	tctatgattc	tctcttttac	240
tttctaagac	cgaaatgatc	tctatccaaa	acggattggg	cacgcttcag	gttgaattat	300
atcttacact	gaaatacgcc	ccacggcaga	ctgatgatgg	tcttacatac	tgcatctgta	360
cggagtagtc	gggcgattga	ggatgtagcc	gtccagcttg	cggagttctt	tttcgaaagt	420
ttctgctacc	tegetgetee	attcatcgta	gcagctttgg	tacgcagctc	ctgcacctcg	480
atgtcgttta	attgccaccc	agttcctcct	gaatcgtctt	gatttgctgc	tgcaggaaga	540
ctctttctgc	tgcttgtcca	tctcctcgcg	cgtcttcatc	tgaatagagc	tttcagttcc	600
attacctgaa	gctccttgtg	caacaggtag	agaagacata	gccacgatcc	ttcatcttgc	660
tgatttccag	caattcttgc	ttgacgctat	gctcgtggat	atattggccg	atgcaaagtt	720
gatctgatac	atcggttctt	gttccgtctc	atcgagagga	taagctcccg	agggggtctc	780
tcgacatcag	ctccatcatc	ttcagactca	tatcctgtat	ggtggagacg	agtcttcgaa	840
ctcgtgatct	ttgttcttcc	cggggagaat	gtctgggagc	agttcacgcg	acccttcata	900
aaaggttccg	tagccgttat	ctcctgcagt	gaaatcgctg	gcggccttgt	acgatagccg	960
tggtagtacc	atcgggcatc	ccagcaccct	gatgatttca	gccacgaccc	cgacatcata	1020
caaatcggcc	gaatcggttc	cttcacatcc	atattgcgct	gtgaaacggc	accgaaatga	1080
caccettett	ctcacgtagc	cggatcactt	gagtgattt			1119

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...454
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

catccccggc	aatcccagcc	acatatacca	gaacataggg	gctacaactc	atcgctcaga	. 60
ttctccgaca	aagtctccaa	agctgccgtc	ctgacttctg	cqccqacaqa	gcagccgtat	120
cgcgccctac	gattcgcgtc	acctgttgcg	cccttcttca	agcgaacgat	cgactgcttc	180
gaataccata	cgtactcacg	aataagggta	gtacctqcca	aacagaagaa	aatggccgat	240
agccaaataa	gagaagccac	agcaaatgca	acagcaatcc	ggaaaaaatc	gtccgcaaaa	300
tggtataaac	acagacaaaa	acaagtccca	agaggatcaa	taggtcaaaa	gaaaaacggc	360
aacgatatag	aacaccgaca	tgaaggcgcc	ttcacctgcg	gtagtttcct	ttattcaatc	420
tttctctccg	atgcaatcat	ggaccgaagc	cgac	5 5 		454

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 982 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...982
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

ccgtcatgct t	tgatggagag	cgtatcggta	tggatgtact	caataccatt	acqacqtatq	60
taaggetetg a	attgacaatt	atgcagaagc	caatgattcg	aaggcttcaa	ggaagatetg	120
atgcgtgcac t	cgcgataga	atctccttca	cgcaagaaat	attcagaggt	aaqaaaqcaq	180
aagagctgac c	gatatettt	tcgatgaagc	ttacaagtct	ttccaacgta	agatggatct	240
gatcgagaag t	ggcccaccc	tgtggttcat	caggtattcg	agacccaagc	cacctataca	300
agcgcattct a	atccccatt	acggatggta	aacgtgtcta	taaataggat	gcaatttgcg	360

tgaageggat	gaaactcaag	ggaaaagcat	cacaaagaat	ttgagaaagc	tatcgtactg		420
catactateg	atgagtettg	gaagaacatc	tgcgtgagat	ggacgagctt	cgtaattccg		480
ttcagaatgc	agctacqaaa	acaaagatcc	actacttatc	tataaactcg	aatcttacga	A	540
ctqttccqca	agatggtaga	agccatgaac	cgtaagaccg	tagcgatcta	atgcgtgctc		600
		ccttcccaag					660
		gtacggcatg					720
					gctgctcccc		780
		ataagatcgg					840
					aatcaccgac		900
tatggtatag	aatagtctgn	gattctcttt	tatttttct	ctctacccgc	atataaaaaa		960
	ctatctatga						982

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1317
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

```
tcactctcca cttcgagcat attgcccgcg aagtgctcca cctgctccga ctaatggcta
                                                                        60
tgatgcggtg tccgttagcg gtcaggctat tcaccaccta ctgcgctcgg cttcgtccct
                                                                       120
                                                                       180
gatgcactcc aaacaaacga tcgcatacgc gaagccacac acatcatcac attggtatga
                                                                       240
tagatgggag caccatcgca tctgtggcgg taaaaatcaa tcctttgtag tccaattccc
gacaaattcc tctaatacct tcggattggt acgttcggaa gagcagcagt aagcatacga
                                                                       300
                                                                       360
ttgaccctgt ccaataccat actgcccgtg ccttcgagaa aacattgtcc cgctcgtagc
cggagagatt gatgatacga tccacccctt cctttcacca acagtagcca gtacgggcaa
                                                                       420
                                                                       480
tttccgctct tgctgcctgt tggtgcatac atgggataaa gcaccaattc gcctgtgaca
                                                                       540
tgcgtgctga ccaattgttc gggaatatcg aatccggtgt atgaggtgtc ttcgaatccg
                                                                       600
aatgacccat acatctaccc cgtattcgcg caatagattg acgtagtttc aaactctttt
                                                                       660
ttcgcttccc ttgctactgc ttcgggtact cccgtttttt ctggaagctg ttgttctgg
                                                                       720
ccgtttcggc attaaatcca aaaagaccgg gcgcaccatc agcacccggt tcgtggcctg
                                                                       780
cttgcgaata agagcatgaa tggttactct aaaaccttga tggattcctt gataatctcc
                                                                       840
acggttgcgc cagctcctca cgtgtgatac aaagtggcgg agccaagcga atgtatggcg
atgcgtcggt ttggccagaa ggccgcgttc ggccattgcc tccacacgtc ccatgcctcg
                                                                       900
                                                                       960
tgtctattgt gcggttcgat gacaatagca tgagcatacc tcgtccgcgg accaacttca
                                                                      1020
atagaggget ettgattttg geaactetee tetgaaatae tgeeceaget eeteggetet
                                                                      1080
ctccggcaac gttcttcttt taccaccgta agggcagcca tcgccacttt gcaggcaagg
                                                                      1140
ggaatccccc gaaagtggaa ccatgctcgc ccggcttgat cgtaagctaa cctcatcgtc
                                                                      1200
tgccaatacg caacttaccg gcaatacccc gccggaatag ctttaccgag cacaacaata
                                                                      1260
togggacgaa cgtcatcatg atogogoaga gcatcogtco cgttcgtgcg atacoggtct
                                                                      1317
gcacttcatc agcccaaaga gggcatggta cttgcggcaa agctctgcag cacgacg
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...502
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

gcccttcctt attttggaag ggatggtacc ctaccctcct gtaaagacat gcatataacg 60 agtgtgaagc tggtcggcag tatgctcttc tatgtgtcgt agagtgaacg catctcctgc 120 ataaaagagc ggaatatctc tatacgacta ccgaatgccc cagaatgatc cggaccgatg 180 taggattggg gagatactcg gatagtcgct ttcgttgata ttgagaccga cacccagaat 240 getgtgtega ggttgetgee egteaggetg tgetegatea gtatgeetge tattteeegg 300 tetecatagt atatategtt eggecatttg atgetgagea tetggeagaa ggaagaaggt 360 cgtagagtgt atggagcacg gagagtgcac acatcgggag agatcgaatt gctgctgtgc 420 aggaagcatg gtcggcctca gagaacggaa aaggtcaggt tcaagcccgg agacgcgaac 480 cagctattgc ctgctgtcct cg 502

- (2) INFORMATION FOR SEQ ID NO:63
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 674 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...674
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

ggaaaacagt cggctgtacg cttccacctc cgccacgtcc gcacacaggg gatctgatcg 60
gaaggatgac gggcaaactg atgatgaagc cggaagagtt tcttccctgt tggccgactc 120
cgctttctgc gattcgctgg gattcgacca cactccatcc gcagcctttt tctgcccgaa 180
acatacgaag tggattggac attaggccaa aggacttggt tctgaggctg aaagagatac 240
tacgacgcta ttggacagca gagcgacgga gtctggccga ctcattgggg ctgagccgat 300
ccaagtatcc attatcgcat ccatcgtgga ggaggagtcg ggaaatccga tgaatacccg 360
cagatagccg gtctctatat ccgtcgcttg cggaggggat gctcttgcag gccgatccga 420

cggtgaagtt	tgcgatggga	gcttttccat	ccgtaggatc	ctgaatgtcc	atttgcagac		480
ggattccccg	acaacactta	taaaaacgaa	ggactgcctn	cgggcccgat	ccggctaccc		540
ataccgcgac	catggacagc	gtgctccgag	cggatcggca	tggctaccgt	atatgtgtgc	-	600
caaggaggac	ttctccggcc	gtcaccgttt	tgcccaccct	atgccgaaca	ccaacgcaat		660
geggettete					-		674

- (2) INFORMATION FOR SEQ ID NO:64
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...789
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

```
cettettgge atggeegget ttggacaegg getteaegat gttetegatt ggtagategg
                                                                        60
ataagagacg cgagtattct ccgtcacgga tttgtcacga agtcgatctt accggcagca
                                                                       120
tecaeggtea egiteteeag eagegeatge gaegaatgge attgtagatg teeggitegt
                                                                       180
tetegegget caggitatea cettggegta geateegeet tegaagitga agataeegte
                                                                       240
ettgtecage egtgetegte ategeegate agettgeget teggateegt aetggegtgg
                                                                       300
tettgecegt accggacaga cegaagaaga tageegtete etttegteea tgetegtatt
                                                                       360
ggcggagcag tgcatcgaag ccataccgcg caagggagca ggtagttcat gtaggagaac
                                                                       420
atacettet teateteace gegtaceatg tgtteaggat caettgeace tteteggtea
                                                                       480
ggttgaatac acggccgtct cggagttcag tcccagctct ttgtagtttt ccaccttcgt
                                                                       540
ttggaagcag tcatcaccac gaagtcgggc tcgccgtagt tggccagccc tcttccgtgg
                                                                       600
ggcggataaa catattettg acgaagtggg cetgecagee acetecatga taaageggat
                                                                       660
tttcaaccga gagctttcgt tggcgcgcag aacgtgtcca cgacgaaaag acgcttgccg
                                                                       720
gagagetget ceaegeeage tttttgatae tetteeaege etteggagte aeeggtttgg
                                                                       780
tgtcttctt
                                                                       789
```

- (2) INFORMATION FOR SEQ ID NO:65
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 685 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

geogtetggt tgaaaaggge aagatgtetg eegatgagea geaageegta tggetegtat 60 ccgtacgacg atggacttca atgacctgaa agatgccgta tcgtgattga agcgattgcc 120 gaagaaatgg aaataaagaa acaggeetea gtgetgtgge ggaagtggta agegageaat 180 gtatcatcgc taccaaacat cttcattgag tatcacagct ttggcaaccc gaactcccta 240 ccccactcgt gtgatcggaa tgcacttctt caatcccgtt cccgtgatga aactgtagaa 300 gttatcagtg cccagcaaac ttcggacgaa gtgatgaagc aggactggac ttgtgcgaaa 360 tgctcaagaa aacagccgta cgcgtgaacg aactccgggt ttcgtcgtaa accgtcttct 420 cataccgatg atcaacgaag gatcggagcc tatgcccgac ggtgtggcca gcatagagga 480 aatagatcag ccatgatgct cggtgccaat cacccgatgg gccctttggc tttgggcgat 540 ttatcggttt ggatgtctgt ctggctatca tggaggtatt attcaccgat tggtgatgcc 600 aaatategte eteateettt gettegeaag atggteggea ggaeagettg geegaagaee 660 ggcaaagctt ctacgactat agcaa 685

(2) INFORMATION FOR SEQ ID NO:66

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 616 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...616
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

tettecaaca atttggatat gateategee atgaagetgg cegeetttee ggeaaagett 60 ggcgttcgga tgctacagca gtgaaagcaa ccgacataac gaaagtgcga cagtagatgg 120 agetegaate atgggtaegg atacegggte atageteegg gaegettgge agatetgtgt 180 ctgatacgtc tggacacccc gaaaatgact ccctgtcaca acttcatatc caacttggtt 240 tattcgccaa tagcagtgca gtggatacga ctattgtaga tgggaagatc ctgagcgcgg 300 acgtaaagta cccggagagg aagccatatt ggccggcgca gctaagctgc atacaaactg 360 atggcaaagg cccacaaaac acacgaatga aatataagca taccgcatat gaaactccaa 420 gaacagcatt accacgagge acatetttee tgteeteteg tetaceggge gatgeeaaaa 480 cggctataat ctgggtagcg gcttaggcga actggccgaa aaaatcgaaa acaagaccgc 540 atcccctaca atgagatacc tcatttcgcc caagctacgg ctgtagggac aagggtaata 600 tcatcggagg aatctt 616

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 710 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...710
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

tcaactatcg	tccggattcg	tacgttctca	ttcctcgcgc	tttgtacgag	agggtagagc	60
cgactattgg	ctgaggactg	ccatccacct	gccggacgag	gcaagggcgt	agccgtcatg	120
gagtacaacc	tgcctcatca	ggataagtgc	tgattttggc	ttgggacaaa	gcctcttcta	180
tgaattncta	agaaggcaca	gatcggaaca	gagttcaccc	ccggctttat	ccccttttc	240
aaagaacgga	gcgacagagc	aggcaacata	cggccaaaag	agttgccctc	aatcccggca	300
tgacaaactc	gacctcttcg	tattcgaagg	aggtagtctg	ctcttgccaa	tacatacagc	360
ttcacggaca	atcaaggcgt	tegetecate	gagaggaagt	ccttttctat	ctggtcaccg	420
tctggaagag	cttacggttg	gtatagagca	tgaccgtatc	gttatctgta	tccaacaaaa	480
tatccgcgac	actctgtcgg	aaaagatgat	ctcaggcaaa	tattggagcc	gttcttccgc	540
atatcgaact	gtgcaaagag	ccggtgtaac	gccatattcg	aactctctct	ccacttcttc	600
ccctatgcgt	gtaatcagag	gtaaatacgg	acacagggtt	tcgatgtacc	caaaagcttc	660
aatgcccgtc	ctacaacgga	ttttgcaaag	agaacctctt	caacatccta		710

- (2) INFORMATION FOR SEQ ID NO:68
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...489
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

ccgaatttgt	gaaaataaat	gattgcagta	tgaaaaacaa	tttttacaga	gaagcttatt	60
ggcaatgagc	gttttttcc	teggegeatg	tgtccttttg	gacagaaaaa	cagtgataag	120
caggatgatc	cgatcttgct	ttatcctttg	ggactacatg	gtattaccac	acaagtgaaa	180
aaacgagtat	ggactccctt	cgtatttcgg	gtatatccgc	catcgtgtcg	agaagaatat	240
ccaaaaggcg	aataccaagc	tcaagagatt	ccagtgggtc	aataaagatt	ggacggtctt	300
gagaccccga	tggagccttt	ttacctatat	agaaaaggag	gtaggcctat	gttgtagagt	360
ctgacggctt	gcgactgctc	tatgatetea	cacagaggtt	ggcgacgtta	taccccttcc	420

cgtcaaccaa ggtacagtcg tgagggettt tetcatggga cgacaacggt cattgaaaaa 480 tecacaatc 489

(2) INFORMATION FOR SEQ ID NO:69

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 656 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...656
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

ggcaaacgta ccgcacctga ccaagaggag tccgcatgtt ctgagacacg cttcgccacc 60 gaaatgotca accacggago agatotgata toggtcaaga acttttaggg cacgacagoo 120 tttctacgac ggtgcaatac acgcatattc gttcgaacaa cttagacaga tgtataacgc 180 tcatccaagg gcaaaaaaga aacgaccatg acagatgtaa gaatccaagc tctgcatttc 240 gatgcaccga ccaactgaaa gattttgtac agaagaaaat atccaagctg aatccttgtc 300 cgatggaata acgggagccg aagtcgtcct caagctcgtc aagctgagac cgtacaaaac 360 aaagaagcat ctatcaggct ctatatcccc gggacgactt gttcgcggaa aagatagcag 420 acacctttga ggaagctatt gtctgacagt cgatgcactg aaaagacaga tcgaaaaaag 480 gaaagaacag gaaaatagga caaagaccaa aaagattcgt cgaatgtttg gcgaattaga 540 aatgtcacta aatttgcage egattegeet teeettaate egeatgaget aagetgtgat 600 tttagoggta ataagtcagg cacoggaacg ogaggggagt taccagagtg gocaaa 656

- (2) INFORMATION FOR SEQ ID NO:70
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 593 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...593
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

agaccagccg	agccgaaact	cctctgcata	gtgcttgaaa	atggtatcga	ctgcgatata		60
				ctcctcttcg		A	120
cgctcttgct	catctcgaag	tatcgctctg	tatggctcgg	tacgattcct	tgtcggggat		180
ggattccccc	catcggtcac	ccaccgcgcc	agacaatgat	tgtccttgcg	gacgatccat		240
tgcagctttg	tccgaagcct	actttcaaac	tgatgtctat	attgcggtag	taggtccngn		300
ccantcgtgc	caactgttca	tcggcaaagg	tgtagtctat	ttccctttgg	ctacctgcgt		360
gatcaggtct	tcggtcgtga	gggtatctcc	gcgaggatca	gcgaatcgat	acctccccc		420
acttcttcgt	tcaggtgccg	ggccgatcgg	catagcgagt	atgtgccatg	actgtaacgg		480
gcttgccgat	agatctgtta	cgttcgttat	acgtggattg	ccgtcgctgc	gttgcaccat		540
acttgtcccg	atatttcttc	gggaccaacg	aagagatact	tctgcttacc	ttg		593

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...540
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

```
ggactgttga tgcagtcgat gatgaaaacc taaacggacg aataatagaa atttttaccc
                                                                        60
caatgatact cttggccccg aatcggaaga gaaactaaaa ggttgggggt tttactctc
                                                                       120
asagcctccg asgatttcgs tcttcgcasa ccastgasat atccatcgsc ttasctgttt
                                                                       180
tcaaagattt ggctgttcaa tcaccgaaaa gcattgtaat ttatacggtg agacaatctc
                                                                       240
atacgtgaaa aaatgacact gaaaaaggga gacttaatga ccaagccatt tttcaaagnc
                                                                       300
ttttntaggg taaaagaata agagcatggc aaagcgaata atccgaggat aggagacgtt
                                                                       360
tttgaagtcc aattagataa ttgcaagaag tatttcagta catcgcaaat gacatgacac
                                                                       420
agctcaacag tagcgtaata ctacttttgt ggaagaatac cccttggact gttctccgat
                                                                       480
cttagaaaat ttacccgcgg gtaagggtga ttttatgcac atacagtcct ccgatgggga
540
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

gagaatgatg	cacgccgtgc	catcgaagag	ctgttcgatc	aggaattcca	ggtcgcaagc	60
tgatcgtcaa	agaggcattg	gaacgtcccg	agcgtgctct	cgccgtactt	tccgacacga	120
agatcgctat	tgatccttct	cccacttcgg	caagtcgtac	cacaacgccg	atacggcttt	180
ccctctgaga	ggtettetet	attattctaa	cgacacgaat	tacaagacag	gccqcaqqca	240
caccacatac	ggtgttcacc	tgcggccttc	ttgcatctgc	ttgtaccatg	acageettqt	300
cacaaaccat	cccaaccgca	actatatacg	gctctcaccg	aacttccacc	ccccgaact	360
tgccatccgc	cacagagcag	atagcatctt	cctcaataga	ccatagtatc	ctctcatgtg	420
agaccatagt	atcctctcat	agagaccata	gtatcctctc	ataggagacc	atagtatect	480
ctcgtatgag	ccatagtatc	ctctcatagt	agaccatagt	atctctcgta	tgagaccatg	540
tatctcttcg	tatgagacca	tagtatecte	tcataggaga	ccatagta.		588

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 646 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...646
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

ggacttatgt	gttgaacgaa	agcttcgata	cgcaaacgct	tcctaacggt	ggacaatgat	60
cgatgctgat	ggtgatggtc	acaattggct	atctacaaaa	acgtttacaa	cactgctact	120
catacaggtg	acggtgctat	gtttagcaat	catggacagc	tagcagtggt	gcaaaaattq	180
atttgagtcc	tgacaatatt	tggtaactcc	taagtttacg	gttcctgaga	atggtaaact	240
ttettttggg	tttcatctca	agagccttgg	actaatgagc	attatggagt	gttctgtcca	300
caaccggaaa	cgaggctgca	aactttacga	taaagctgct	ggagaaaccc	toggatoogg	360
caaacctgct	ccgatgaact	tggtgaagag	tgaggagtaa	aggeteegge	accttatcag	420
gaaagaacca	tegatetete	tcctatgccg	gacaacaggt	gtacttggca	ttccgtcatt	480
teggetgtae	ggtatattcc	gtctttatct	tgatgacgtg	gctgtttctg	gtgaaggttt	540
tccaacgact	acacgtacac	ggtatatcgt	gacaatgttg	ttatcgccag	aatctcacgg	600
caacgacatt	caatcaggaa	aatgtagctc	cggccagaca	actact		646

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 700 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...700
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

gggtgtataa	gttaatgctt	cctttgtaaa	atttgaagtt	gttataaagt	cccttttttg	60
gcaccttgtc	cagcgagtgc	tccaacaaac	ttttgaagtc	aggtcttcct	accacattcc	120
caggcctcca	gagattggat	tggatataat	aatatcaagt	cccagtttat	cttcttttat	180
tgttccgtca	attccccgtc	tccacttttg	cctaatgctt	taccggcatc	cttgatagaa	240
cctcctatcc	cattttgact	aataattcga	caacaagcct	ctcaaaaaaa	gcagtgaaag	300
gtcaatgact	ttattaagta	attcggaagc	caatgatttt	ctgttctttg	atatgctttg	360
tcaaggacct	cttcaggtgt	ttgttcgtgt	atttttctgt	tatggattct	tcttctgttt	420
cgccgtcatt	tcgataaccg	tctgaaattc	tataaacgcc	ggaaaccgtc	ttaggtattt	480
tgtgtctatt	ttgggggatt	cttcgaaagt	atctctctgc	caaggtcaga	aattataaga	540
tcgctcgttt	aggcgaatca	agaaggccag	ccttctttag	gtatgttctg	cccagccaac	600
gcgattgtca	aaaacagctt	tggagccact	tgccaaggtt	cctgcgttct	tcgtccgtga	660
cctcaaatcg	gctgccaatg	ttcgatatat	ctctggattt			700

- (2) INFORMATION FOR SEQ ID NO:75
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...574
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

cggcaacgct ttt	catcgta ttagggacgc	tgaccaaact	gtatggtatg	ttggcttggc	60
tttcttcccg ttt	gtgaaaa gaaaaggccg	ctatttggtt	ggctttttgc	atggttcggt	120
ctgatcggta tct	tgccgat gttgtttgag	gaggttctta	tgcccttgag	cagtatatga	180
attggtttgc tag	cctggca cgaagaatgg	ggagaatctg	ttctccctgt	atcaaaacgt	240
ttcccgctcg gga	tggttag gaaaatgacc	ggtattgccg	gctactccga	cttgtgttgt	300
tagtccccgg act	tatecta ttegetette	ctttcctccg	attagtcagt	acaaggctcc	360
actctttcgg atg	agcatat tggcttcgac	tegettttea	ccgttttatt	cagtaccggt	420

agegaatega gtaettatat etagegttgt tgggtgtegg tatetggtte atacategee 480 ecaaagggaa eegaeegge tggatattae aetettagte ggaacaetat teetetett ttategeega eegatetgte eetgeggete tteg 540

- (2) INFORMATION FOR SEQ ID NO:76
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 629 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...629
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

gactotaccg cgaaactata gacttttacc ccattcatat cgtataaaga gcttcctgcc 60 ctaaaagaga ctcggggatc tcgacgagcg catatcttct accggattgg gatatatcct 120 gacagtggga gcatctactg ccaagttgat gtcggacttc cttcgtatgg aagcatattg 180 tcagaatcac cgttgagtca aatactcgcc agttcttact tttagctttt tccacatcct 240 ttacgtacag atattettet cateagtgte ettgaggtgt tenaaacgae gaaattgete 300 tgagegeetg egeegggaga tagtgtggge aaageattea ceatttegte atttetteae 360 ctgcgatctg attggaatga caaaccaaaa catcagtccc ttcacccccg acagattcaa 420 ggatgtaagt ttgttcgatg acaccaaagg taagcaacgt ccgaattctt ggaaagatcc 480 aaggtegaaa eteattgtea etgeaceaaa gtgttaceaa tagaggattg geacteagae 540 gagtttcgtg atccgattac cgaagcacca aagatcattg agacgaggtt ggcactgagt 600 tccaacttcg tcaggttata tcagaacac 629

- (2) INFORMATION FOR SEQ ID NO:77
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 647 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

+-+	anantaatta	CCACCAAACC	aagecteate	gatcagattt	tctgagcgtt	 60
caatattaaa	Cacatectta	Cyaccaaacc	aageeeeace	gaccagaccc	000909-9	
qcaaacccaa	gagggggtga	atacttctgc	tttatcctgg	tgcggttggc	ttgttcttcc	120
ttggacttca	gcactctqqq	ctgtattcag	tgtcatgctc	ccctgtaatg	ctgtcagtcg	180
taattggtgc	atcotattoo	tacgcatctc	ccagtgtagt	atagtcatct	gtagcccaaa	240
agatateete	tgagtcgtat	ggtcaaagag	gagtetttge	agaagtcctt	cggatgacgc	300
agtagttcat	totcactaat	atcaaccccc	atcttcatat	cgccacgagt	aacctctttg	360
ageageeeae	2000000000					420
catttqacaa	gcagtggttg	tcaaattact	gttaccatat	agaattgcca	ttttgggeae	420
agattagaaa	taggcacgac	aatctqcccc	tactcttagc	caccggttgg	ggacatcacc	480
			statassata	attacataac	casaddtaca	540
aggaaaaagg	ecteggtett	ttategitti	acctadactc	attacataag	caaaggcaca	
agttaggggc	atactaacga	agggaaatgg	atatttcttt	accgagtaat	caaagtgcaa	600
		gatttccggg				647
Cayacygyac	aaacagcaga	gaccccggg	caccaggeog	33		

(2) INFORMATION FOR SEQ ID NO:78

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...450
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

tttcagcaaa agccggatag agato	ctgtcc actcttcatt	ttcaccggcn	ccgccgcgcg	60
caagttetea geegtggaac egat	tattcc tgcaggaaag	aagccgttat	ctcaagcatg	120
ccgccttcca agaaagagaa aaacc	ctttgg catgetettt	ttcctgctca	gcggtttcca	180
tgaaaactcc ggcaattgtt cataa	accete tttettggca	acacttgcaa	agaaagtata	240
qeqeqeeqaq ettgegatte teeg				300
ctttaatact cttattcatt tctg				360
atcacaaaaa taggtactac cacte				420
gataggtect eqtatetttt taage				450
gacaggood oguateria amag				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...543
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

gcctgttcgg	actacgagtg	ggaggggata	catatecett	tagtgtggag	agtacaagcg	60
gcctacattc	gaagtcggcc	tccggagtcc	cgacgctgat	atgctatggg	cgacaccctc	120
cgcatacgag	gcgaagccaa	gacctttccg	gaatcggtat	gcgaggagct	acggtgaact	180
atcggctgag	cctgacccct	atacgcgttg	gttggtgggg	tagacctgtg	gccgataggg	240
tcgtaagacc	ggtgaggcag	tggtagatga	atcggggtac	ttcgtcatac	ctgttcgctg.	300
tctcggccgg	aaggacggga	agactattcc	tactgcctct	acagctatcg	gtggatgtga	360
ccgcccccgg	tggcgagacg	caggccgccg	tatccgaata	cccgtgggaa	aagaacccaa	420
gagggtggac	gtcgaagtgg	gaaatacatt	cgtgccaacg	aagacaactg	gcttgccacc	480
tetetgeegg	tctgacattc	tcccttacca	atacttttcc	ggacagacgg	tggagggatc	540
atc						543

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 671 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...671
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

gcaaacctcc	gacaaagaac	tgcatctgca	caatgtgaaa	ctggctatgc	aagggtggag	60
cgacatagct	ccattaccct	cagttcgcct	ttccttgagg	agcactgcat	ggcgagttca	120
cattgtccaa	gctgccttcg	atgctcgagg	agtggttggc	gcacatcttc	ctgcacttgc	180
gggccatagg	tcgcagcaag	agtgccgact	gaggatgtcc	gtctgcgttt	ggcgttggac	240
ggctcttgcc	caaggaagtg	tgcagcttct	tccggttgcc	tttggccgaa	gcggttctat	300
caagatcagg	gcagcctatt	ccgaattgct	tcgaagcctc	gattgcacat	tegtacegae	360
aggctcatga	ctatgaacaa	agagctacgg	gaacggaggt	gaccttgaac	tcatccaccg	420
gcaaggccga	actcatctgt	cgtccgactt	gtatgtgaat	ggcgatgcca	cgacacgaga	480
cctcaacctg	aagcatcagt	ggcaaacgac	agcatccgtg	cccgactgga	tatgggacag	540
acaagcgagg	agcgaaaaac	ggatttatat	cgctgctcac	aaacttcctc	gggacgagga	600
ctcatcgctg	aatactcata	tcggtctcga	tegetetegg	cacgcatcgg	cggtatgagt	660
ggcagatagc	c					671

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 999 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...999
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

agtoctatca gatocgacat ttatgttttc ggacggtatc cgatgagtat tttatcggat 60 atccggggct ctcctcttct tctttttgta cccacatcac tttttctacg cgagttcttg 120 cacatetacg getegtgttt tteggaaaag tggegegaga ttttttegt tetggegegt 180 aaaaatttta cttctccgcc aaaagcaaaa ttttcccgcg ccacgttttc cgagacatga 240 ataaaaaatt ttccgaacgc aaacaatctg aacggacagt ttgccatgta ctgaaaagtc 300 gttgacacac ggaaaggttg tgaagatcga tttccggctc tgccgatctc cctttcccac 360 taatccgaca gatactgatg cccgcttacc ccaaaaaaga gggagaaaaa cgcttgtaca 420 actaaaaaa gatactacct tgcatcgcaa tcgcggaagt agctcagttg gtagagcata 480 accttgccaa gttagggtcg cgggttcgag tcccgtcttc cgctccaaga ggcagtagga 540 tgcggcctat ggcggtctcc tcatcctgaa aaagggtgta tctttccaga aagatcggtc 600 gataacatag acgcccgggt ggcggaattg gtagacggct cgtttcaggt gcgagtgttc 660 aaaagacgtg caggttcgat tootgtoogg gcaccgacta togaggaaaa gacaaacaat 720 ttttttgcgc gggtgtggaa ttggtagaca cgctactttg agggggtagt gccggttacg 780 gtgttgagtt caaatctcat ctcgcgtact tttaatgaag aggatgttca ttcattgggc 840 atcctctttt ttttgtttaa ggaaggtgcc caatggcgtg aacggtataa atagatatct 900 ttaatetttg tataataaaa aacaggeaga agaageagea ggaaagegag cateecacaa 960 gtggcgaagc catcatcatc aaggggcacg ggtcaataa 999

- (2) INFORMATION FOR SEQ ID NO:82
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 548 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...548
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

ttcggagcgc ata	totocot gttoggottt	tttacgttga	agaatgcatc	gcatgcagtc	120
gtaaaacget tee	atatete ateaetaaee	gatgaggaac	ggctccgatq	gttttccatt	180
tettttggag tte	ggcaagc gagtagaggt	ttctttccag	tcggaactct	cctgaagget	240
ctccgttctt ctac	ccatggc cagettette	ttgtagttat	cggtcagete	ttcagtttgc	 300
ctttgaagaa agct	tgttttc ttattgaaat	aatcgtcaca	tgcgcgcgga	aacgctcgta	360
gatettetea ttgt	togotto tgogagoata	gctatagtct	tccacttggc	ctgaatetet	420
agtacggcct tcgt	tttgctc gcccatttgg	ccagcgagtt	cagaccggag	gtatctatcg	480
cttccatttc tcac	caaagca atgttttcgc	agccagattc	ttctactcac	gcatcttttc	540
ttttcgaa	_		- 3 3 -	3-4000000	548
					240

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 668 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...668
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

gggtgggts						
ggeteegata	caggaagete	tctctcccta	tggcaatacg	aagcaaatca	cgaggagatt	60
atccgcgatg	ctatccatgc	cggagcaggg	tacaaqqcat	acttctgcgc	tacttcaatc	120
cgatcggggc	acaccccaca	acacatacaa	agagetteet	2222222		
3 333		gogoacacgg	agageeeee	aacyyaytgc	cacagaatct	180
gatcccttat	ttgactaaac	ggcagcaggc	atcagagccg	aactgagcgt	cttcggcgat	240
gactagacac	decedacade	tettatatee	aggactatat	atatata	gattggccaa	
	3 3 9 9 9 0	coccycacce	gggactatat	ccargrages	gattggccaa	300
agcgcatgtg	gctgccatcg	aacggatgct	gaatgaagag	aaacqaqcqa	ttcgctcgaa	360
gtctttaata	taggtacggg	taggggggtg	2001001			
,	caggeacggg	caggggcgcg	aggtgctgga	gertateegt	accttcgaac	420
gggtgacagg	cgttgctgtt	ctcatcggat	agtaggaagg	cacassaaca	atatogasca	480
aatstaaaaa				- 9 - 9 4 4 9 9 5 9	acaccgaaca	400
ggcacgggcc	ageegaagaa	agccaatgag	gtgttgggtt	ggaaagcttt	ggagtcgttg	540
aagacacact	getgagtgea	tagcattagc	agcaacgctt	atcagagagt	22+22-2-	C00
	J J J J - J	- 55-500990	ageaacgeee	gccggagagc	aateegeage	600
ccattaacgc	acccgatacc	ctatcttctg	gcagatgaca	tcctatcgac	caaaatcact	660
tacctgac			-	3		
5						668

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 647 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...647
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

60 ggaaaatata ttcgcggacg cattattgcc-acctgtccgg ggcacagcac-aacaacaaga 120 tggcgcgcct gattcgcaaa gaaatcaaac agaacgaaca caggcccctg tctacaatcc 180 gaacaaagag ccgatcatgg acatcaacgg atcaaagagc ttctacccca ccgctatccg 240 ttoctattgg togatagato atogaagtag ggooggacta tatagtogga gtaaagagog 300 tttccgcaac gaaccatttt tccccggtca cttccctggt gagcctgtga tgccggagtc 360 ctgcaagtag aggcaatggc gcaggtggga gggctcttgg taccaatacc ctgaccgagc 420 cttcgagcta ctccacatac ttccttatga tcacaaagtg aaattccgcc gtaaagtggt 480 acceggegae actttggtgt taageteaga atgattteeg agataegeag aggagteget 540 aatatgcgcg cttagctttc gtaggagagc agttagcctg tgaagctgaa tttatggcaa 600 gataatccag aataaagaat gatgtcagag acaaaaatca gtccgttgca tgggtggatc 647 cgcatgccga agataggaag taggtgttga gataggtcca ttgccgt

- (2) INFORMATION FOR SEQ ID NO:85
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 631 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...631
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

60 aaagtccaag gaagagttgt ctgcttttct cggctgtgag catatcgagg ctgcaaatgc 120 ttcgtcaage aggageaatt gegggegttg gagaaatate gtgeeagtge cacaegetga cgttgccctc cgcttagatc cttcggaacc gatgcaatat gtccgacaag ccgagggtgt 180 gtacaatgct ctcaaatccg gcatctctat gggctncctt ncgcagggta tatggaagta 240 300 cgatatetea tgeactegtt tecatggeaa aageeeatat tgetggggaa etateetatg 360 gaaaaagatt ttggattcag aggtttccca tcgaatagca cttgccctca tactctgtca gtacacctgc caaaacgtgc aggagtgttg attgccacag cccgaaggtc ccgttatggc 420 480 aaaaatotot ootttgggaa tttoagtgaa agacogtoca atgotttoac ttoogtacto 540 ccgtggcgat tgtaacggcc agattgcgaa tagagatcat ttgcctaatg gaggaatctc gtttcgtccg tctctttgat tatgccggac tttacggatc agatccttcc ggttagtcgc 600 631 tegggaceaa tttettggea tgtacceagt e

- (2) INFORMATION FOR SEQ ID NO:86
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...498
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

aagtgctgac	gggccaagac	agttgttacg	ggcaccggaa	gccattcgtg	cactcgtgtt		60
cagggcacct	ggtatctaaa	gacggtacag	ttgcctgcgg	tactaagtat	gttgccttcc		120
greacttegg	ctgtacggac	ttcttctgat	caacctcgat	gatgttgaga	tcaaqqccaa	•	180
cggcaagcgc	gcagactcac	ggaaacgttc	gagtcttcta	ctcatggaga	qqcaccaqcq		240
gaatgactac	tatcgatgcc	gatggcgatg	gtcagggttg	gctctgtctg	tcttcggaca		300
accgggatgg	ctgacagete	atggcggcac	caacgtagta	gccctttctc	atggaatgga		360
atggetttga	atcctgataa	ctatctcatc	tcaaggatgt	tacaggcgca	acqaaqqtaa		420
agractacta	tgcagtcaac	gnnggttttc	ccggggatca	ctatgcggtg	ntgatctcca		480
agacgggcac	aacgccgg						498

- (2) INFORMATION FOR SEQ ID NO:87
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 647 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{47}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

ggattttctc	aacttctctc	contantata	+-+			
	aucticigic	CCatcatctc	Latagaagge	agccggatga	gccttacgat	60
greaataega	tgctcggaca	gctcaagcgc	gcacaaatga	aaaagtggtg	caggatggct	120
ttgagaatgg	ggcactctat	aatgacggct	actcaaactt	accgaggtag	adctdcacda	180
cttcgacgaa	ctcasactat	Cattaggaaa			agoogcaega	
	- coddag ca c	caccygcaaa	accaaggcga	tggcaaagtc	cggtgacata	240
gatataatca	ccaaggtctc	acccatgage	aatacgagga	gaaagagcqa	ctgggaagag	300
gaaaaagaaa	ggcctaacac	ccgaagagaa	aaaacgactg	gacaactgaa	adccasaddc	360
gaccaacgcc	gagaggetat	ttotatooto			Lycoladygo	
5	gagaggecae	CCCCACCCC	cgggcatatc	catecgeatg	cctctgatgc	420
tctatggggc	tgaaatgaag	gtgaggataa	ggagctgacc	attgacaatt	ttgccaatct	480
catcaataaa	agtettagea	agaatttata		***		
cgtcgatgag	ageoccygca	ggaacttatg	ceregeggeg	ttaccaagcg	gtctttcgtg	540

cttcaagcgt tactacgacc ccgacatatt cgtgaggcgg ggaagcgctc cgtgagatgg 600 ctcgtatggc ggataagttc accatcgaag gagcgtaagg gcgtatt 647

(2) INFORMATION FOR SEQ ID NO:88

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...622
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

60 gggatttacg attagacgaa aataggccag gacgtccttg atctcttttg cgaatagaac 120 gaaagcccac cgtatatacg aaaagggata ttgtgtttcg aagtgcttcc tcgaaaactc ggctctgcgc attagtgcgg tacagaaggc gaaatcggaa taaggacaat gctcttgcat 180 gegtegeteg aegateaate egetacegta taageeteea aataeeeega eagacaaeee 240 300 gtcagcgaat acgctcacct acttgtttgt tcgaaaaaac ttgcttgggg attcccctc attgtgagca atcaagctat tggcagcatt gacgatgctc tgttactccg atagttctcc 360 420 tcaagtttga aaagtttgct cccggggaac gatttgaaaa gcccagagtg tttttccact 480 tgggctccac ggaaactgta ttactctgag catcatcccc cacgacgaat accttgcctt 540 totococcat aactgootgg caatcaaata ctgtgcaaag ttggtatoot gatattoogo 600 gatcaataaa taatcgatgo ggtcacggta ggtctgcaag acatccggaa atcacgaaaa 622 aggacattgt tttgaaaagc ag

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 581 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...581
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

tacaaactgg	acgttgtagt	tattccgaca	aacaagccta	togocogtag	gatatgaatg		60
atcgtatcta	taagacggca	cgtgaaaaat	atgcagcatt	atcgaagaga	ttgtacgtct		120
tgtcgaagag	ggcagacctg	tacttqtqqt	actacttcgg	tagaaatata	Casattatta	76	
agccgtatgt	tacgctgcgt	ggcatccaac	Cacaaatota	ctcaatacca	aattaaataa		180
gaaggggccg	agattgtagc	tcaggccggt	Cadaaaddaa	ctatteaast	aaccycacca		240
taaccaatca	tggtaccnac	atcaacetet	ctacaaaaat	tassassassass	cycacgaaca		300
tatcattagt	Scadagadac	accaagecee	cegeegagge	caaaaageeg	ggggtatggc		360
aaccatcaaa	acggaaaggc	testant	acagiggaca	gacagetteg	tggtcgttcc		420
ggccgccagg	gtgatcccgg	tegrecatat	tetatgttte	ccttgaagat	catctgatgc		480
geoceeeege	acagaaaaga	ttgcattatt	gatggatcgt	ttaggtttca	aggaaggaga		540
grycregaaa	actacatgct	nagtaagtcc	gtggagcgtg	C			581

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...633
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

```
gtgctgatga cgttagccgt ttactcattt atgcctctga tccggacgaa cagatctcat
                                                                        60
tgtgacgcga gtgttcgatc gcctttcgga aacactctcg tcggggaaca acgactgacc
                                                                       120
atcaatacgg ctacagaact gaatccgtga ttatggattg gctctctgcc ttggacacca
                                                                       180
atgttgctat cctgctacac tgatgggatt ggtcggaggc ttcacgatga tagcccggtc
                                                                       240
tgattttttg gtcatggaca aaacgcagtt tatcggcatg ctcaaagctt taggtgtgct
                                                                       300
gaagggtege ttegeegeat atteetetat etggetatga tgeegttggt egtggtatga
                                                                       360
totggggcaa tgttttggct ottatactot gotootgcag caacatttoo gotggttgog
                                                                       420
teteettega teetgatatt tetaeatgga etatgtgeet gtteaagtgg aetggetegt
                                                                       480
atggattete ttaatttggg taccetecte gttacettet tgatgeteet tgetecatee
                                                                       540
atattatttc gagaatttcc cccgtcaaag cccttcgctt cgagtaatgc ttcaccaggg
                                                                       600
aatagggtag gtcatctgtc cattcgagac cat
                                                                      633
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 667 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...667
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

60 ggcaacgtcc tccgcagtgc cgaaaacacc tgcattgccc gatatacctc gaggcatgca gcagcttcgt cgtccacggt accgcggacg atgcttttcg tagaaatttg tcgttctgtg 120 ccggtgcaat gcgcgaaacg gaatattatc gagtggaaga taaccgagcg aaccggctcc 180 gatggggggg aatatagttc ttcgacaaag acgttcaagc tcttgcccga tacttttcc 240 acaattgctg tagcaggata aaccccagat ccgaatactt gtagcgtccg actcattgcg 300 aggggtagaa gcgatggtat tgaggacaat ttctttgacc tcttcgatag atacagattg 360 420 gaagaaaaac gaaacggata gtccggccga aatgcccgga aaccaaatcg gagcgaaatc 480 cgaagaatgg attgccccac aattggtatc tactcgaacc catcccgaac tccgccgggg 540 agagagcaac tgccgtccaa actgctactg tctatcagag attcgtagaa attgatcgag gccgaaggcc tgcttcatga agtagaagct gctgtacggt gatgtcttga ggtctgttcg 600 660 ggcaaaacga ggcaatageg ttccgagecg gtcggagget tcaattttcc atcctgaacc 667 aatagca

(2) INFORMATION FOR SEQ ID NO:92

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 612 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...612
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

60 ttgcactcta tctgcgaggc gaagttcccg gattccaccc gctgcagtta accgtgtgac cggccagccg cttgttatga gtgagatggt agaagtatca cgcaaatgat ggaggagaaa 120 180 tgattatgtc agaaacgact aagtgcccat gtacgaggca aaagactata agagcgatca 240 gtatgtgcgt tggtgtcggg ttgcggcgac cacgctgtgg tagtaaccct ccagaaggca atggcgaaat agggatccct ccccatcaga cggcggtaat gtccggtatt cggagttctt 300 360 cccgtttgcc atactatatg aacacctatg gcttccacac catcacggtc gtggtgcagc 420 categogace ggegtgaaga cagecaatee gggettteeg tatggetege ateeggagat 480 ggtgacaget tggctategg egeaaceact teatteatge egtgegeagg aatategata 540 tcaatgcagt ctcttcaata accgtatcta tggtctgacc aaaggccaat actctcctac 600 tragetregeg gattregtate raagagttet rectargeta regetagaaat regettater 612 ccgcagaact gg

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1356
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

60 gattettaga aaagttgatt attaacgaca aaaacaaaat ataaagatga categtaetg 120 actattetea teetgeteat ategetette ettattetgt egtagtggta cagaacteea aaggggggg cttggcagcc ggcttcgatc cagcaatcag atcatgggcg tccgcaagac 180 taccgatttc ctcgagaggc cacttggtgg tcggccggta tcattgccgt tctggccatc 240 300 gtttcactca cttcctccac acgggaaagg tcgatgagag ccaaaacgtt ctgaggaaac 360 ccttggacaa gaaggtgaag gaagaaaaga actctgcagt gataacttcg gtggagatgc 420 cgctgctacg gaatctgccc ggcccgcgac cgagaggcca ctcccgagga ggggcaggca 480 caataaggag gaccggcccc tcatatccct tgcaggagat acggggatcg acagacgtct 540 ttgtctttga cgaggcttga gggcaaagac gtttgtttgg cagggtgccg ctcgccgcag 600 ccccqqqaca aggctcaagg ggcggaacgg acagagcctc cgagggggac gacaagccct 660 tgcgaacgga acggacggac gtacccgaaa aaacgtcaga cgttccgaca aaaacgtcta 720 qacqttttqa ctqaaacqtc tagacqatcq aaqcaaacqt ctagacqttt ttcgcgaaag 780 qtctaqacqt tttqaaqacc cqaccttttq qcaqaaqaca aqaqaqatqa caaaqaqact 840 attetqueeq aatqqqcace qcaaqaqqce qtacaattqa cetqqcetca cgacqaaceq 900 actgggctta tatgctcgac gaggtggaaa cctgcttcgt cccatagcca ccgccatact 960 cogceacgag cgactgatag togtttgccc categoaage gggtgttegg cetgetgeet cccgagetge accacegget tactgetteg agetgeeete gaacgataca tgggegegeg 1020 accaeggage attteectee tegeogaegg cegteegatg atageogaet tegeotteae 1080 ggctggggca tgaagtttgc cgcccatcac gacaacctca tcacgagcgg ctccacgccc 1140 1200 tgggcctgtt cgccgaagga gttaccctgg acaatccctc gccttcgtcc tcgaaggagg 1260 agcactggag acggatggcg aaggtetttg etgaccacgg acagetgeet ettegageeg 1320 aaccgcaatg ccggctgagc cgacgggcat tatcgacacg ctgaaagaga gcctcggcgt 1356 caaccgcgta ctctccttcg cacggagcct tggccg

- (2) INFORMATION FOR SEQ ID NO:94
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

tantantanc	caaatttaac	aagtcgctgc	ccaagggtga	ggccgagcga	ttcgcaagaa	60
theretes	cgaacccggo	gcactcctgc	atctactcat	ccaccaaaga	ggaaaccgcg	120
attegteaag	Caaaagcaag	geacteetge	accegacage	acatanaga	atacaacctc	180
ggaatggcag	cgaaagaagc	tcaggtatag	ctacggaagt	geeteaagae	acgegaceee	240
gctttacgat	ccaaaggaaa	gtagagaccg	aaaagccggc	tgaaccggtt	cettegeeca	
aggacaggag	cctgacaccg	tgcgtgagga	caaacccgca	agagaaactg	caccgtaaaa	300
gaggaaacaa	aggtcgtccc	cgtcaaggaa	gataagccca	aggagaaaaa	ccaaagcaag	360
aagagctaa	acadaaaaaa	cccaaaccgg	agageetgta	caggeggete	ccgttgccaa	420
aagageeeaa	associataa	aaaaccacad	caaccaatca	tgacacagaa	acctcaagaa	480
geeggeegaa	aaacccgcgg	addaccacag	0000033100	adacaccdaa	gaagttttcg	540
gctgaaacac	tecteegget	caagagatgg	ayaaaaaaya	agacaccgaa	gaagttttcg	600
tctgaagacc	aacacgcagg	agccacaagt	gaaagtggtc	ggaaagatga	cctctctcga	
tcaattcatt	cacgcgttcc					620

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1361
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

cataagatca	tgaagcctat	atcaagcgtc	tgaatatctg	aagcactcgc	atgtcctatc	60
caaacattat	caagacctat	gctattcagg	ccggccgcaa	ctccgtgtga	tegteggtge	120
Cdacaadacd	gacgatgcct	caatagaaca	ctctcgaacg	aaatagccaa	aagaatccag	180
gacgagatga	cctacccaga	caagtgaaga	tcacagtgat	ccgcgaatct	cgctccgtca	240
actaccaaa	taatccccca	caccaataaa	tagtacctgc	togcatgatg	tggcgttatg	300
atttatacct	cctcctatca	gcagcactag	aggactacgc	cggcaaagca	aaagacggat	360
accededece	ttagagaata	caacaacete	ccgacgaagg	atgectgeaa	ggggtgtcat	420
ggactaccga	tagacatta	tactggctga	atgacatccc	cgatttgccc	gaagatggcg	480
agecagecge	atageactea	agetagge	caaaggatac	tacctcaaca	gcgagaggaa	540
gattegtgga	gcacagetea	agaacacgcg	anaggaeae	caaatcacac	atcaggagag	600
gagetgeaca	aaggggatgt	agtageegta	gaggccaatc	contracted	atecgagacaa	660
tgacgctgac	cggcaagttg	gtaaaactcc	agatgcgaag	Catcyataca	atacgaacaa	720
cggcgagcct	ttcaaaatat	accgcaagcc	aaacagggcg	atctggataa	gtactgcgaa	
qcaaaqqcgc	gagagacgat	acgatgattc	agtcccgtca	gatttctgcc	gagctgaatc	780
tagaatgaag	atcggagatg	tggagtatca	gggcgatggc	aataaggcca	tttctactat	840
atcoccoato	agcgcgtgga	ctttcgccaa	ctgatccgag	tatggcagag	accttccata	900
tecacataaa	gatgaagcag	atcootocaa	gcaggaggcc	ggccgtatag	gcggtatcgg	960
teettataac	caccaactat	ctactcaacc	tggaagatga	atttcgtatc	ggtgaatacg	1020
actacagaga	ctatcaacac	ttagctctca	atcctcagaa	actcacaaac	ctctqcqcaa	1080
agreeageeg	taataastt	atasaataas	tgcttatgtg	gaagetetaa	gaagatgccg	1140
gctcaaatgc	Lycolcaall	acyayycyya	cycecacycy	944900044	JJJ	

ggctcgtcgt gc	egtettgga gacgaaagaa gtttegtat tetaegttee ettegaggt gateageeag aagaageag tegteeggae	aacaagcagg	gtcaatctta		
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 675 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...675
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

gtgtttttgg cgataaggtc tgaccttgaa aaaaaggatt ctcaaattgt caatatattt teetetatgt ettategatt etgatatata acacaaettt tettttgaag tgggtateag 60 gcttatgttc tatcctttta tgttcatttc atattgatcc ctaatgctta tgtattgtca 120 gataaaatat ggcaaaaggt gtgattttgg ctattttggt tgtgttctca ttctttatgc 180 ttaagatete ageagteeag etgaaceata egetaaetat aagtetatae tetttgaaaa 240 atactggtta agagaataat gatcgtgcat tctcccttgg tcacgtgctt attcctccat 300 acaacgtgga gaaatcagaa atcgagtctg atttgaaata gcctacttga atgtagctaa 360 aatgttttat gacaaagctc ctgcaatcaa tataagacga taagggaata caggccactg 420 aatccgaaga aatcgcctcc atgcaatacc attcgttaat ccgatttagg ttgcttgtca 480 ttgtcagact cttctgttct gagatattta ggatatttct gtgtaaaaag aacagaagat 540 aaaaagaatg atgagageet gaetttgtgt geeacagett ttteetacaa gtaattegae 600 ataatatgat accgt 660 675

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

ggcgaagcat	agcggtagcc	cagctcatag	tegateagte	gctcaggcga	ggatactgtc	60
ctattccggc	ttcggtgtaa	ttggttctgt	taggctcggg	tgtgctaccg	caacagaagc	120
atagggagta	tgagcatcgt	cgaaacttag	gtaagaccgg	ccttcggatt	gaggaagcgg	180
aaggtettgt	ccaaatgatg	tgctgcatac	ttccctgtac	ctcatcatat	tegteegtga	240
taccattate	gtgtagccga	tggtacgata	ctggaggtcg	gcatacatgt	tcagtccgga	300
gtgatctgcc	agttggcttt	ggcaaaggct	gcaccttctc	tttgtctgcc	ctgttccgat	360
aatattcgaa	atcaggaaget	aagggctgat	tgactttttg	atgtaagtga	tacggccgaa	420
ataateteet	ttatagatat	tecegagge	ccgaactgca	aatcccatgc	accggtgtgc	480
cagttaagcg	accgatgagt	cctccgaagt	cattgtccag	atacttctga	cggatgagac	540
cattttcttc	accottcacac	tattttccac	atagggctgc	agtgcatatc	ctttagttac	600
-	atattcgtcc		555 5			627

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{236}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

		antantanaa	atattatada	ggctatcgan	caatetacce	60
ettggetege	actegaagat	gatcatcagg	atactataga	ataasaasa	ccasacaaaa	120
gaagggctta	tcaagagagc	tatgacaata	geggegegag	geggaegaea	~~aattagaa	180
gcaacgggtg	ccctcctctg	tgtggattta	ccgaagcggt	attggaggag	gecattegge	240
tgggatgcaa	tctcgtattg	cccaccatcc	gattettte	aaaccgctca	agcgattgac	
cggcactcct	acgtggagcg	atgcgtggag	ctggccgtac	ggcacggtct	ggtgtatatg	300
cggctcatac	caatgcggac	aacgctccgc	agggactgaa	tgcctgctgg	ccgaacgctt	360
caacttacta	aatacqcqac	cgctggagcc	gcgcaaggca	agctcttaga	actggtcacc	420
ttcatccca	cagagtatac	catgccgtga	ggcaggcttt	gtggcaggcc	ggtgcaggcc	480
atttaaaaca	tacqattqct	gttcgttcag	ccataccaac	acagggactt	tcagagctgc	540
geeeggggea	atccctttat	gggagcgata	agcgaattgc	accatgageg	qaqqaqcqqa	600
tasaataat	actoccccge	tacaggcagg	atactateta	caggetttge	acgcggctca	660
teageetegt	accyccygca	tacaggcagg	coactagees	accatcatco	ctcggcgga	720
teegtaegag	ergeeggerg	tcagccgatc	termore	agagataata	ctacacatca	780
ggcggaatag	tggggatetg	ccttcgccca	taagegageg	ggagacgccg	cegeacaca	840
aggagtattc	ggtctgaagg	tectgtecca	tteggettgg	agggaacggc	egtgaggegg	900
atggctatat	gcggcggtag	cggtgctttc	atgtggcggc	gtcagcacag	gagggtgcag	
acctcttcct	gacaggggag	gcgaagtaca	agacttcttc	gatgcagggg	agcatctgct	960
gctggttacg	atcogtcatt	cgagagcgaa	gaggtggcta	atgagctatt	tatgcgcata	1020
atategeaga	attecetace	tttgccaccc	acaaatcatc	ggttgcaacc	aatccggtaa	1080
ctatttataa	ttagttaatt	gagcatcatg	gctaaagaaa	agatcatqtt	qaqaacgaac	1140
ccacccgcag	aggeeautt	ggcagcactg	accaactcca	aaataccctc	tctgaaatag	1200
						1236
ataagatcaa	gactettegt	gcgaatgccg	cyyaay			

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...911
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

aggttctccg tctcacacag atcgatgtgc acagtttggg tgagctgcgg tcaatcaagc 60 actgcgcaat atcgaagctt tctacgaagc tttcaataac agcctactga taagatgtat 120 ttggaacccg aaaagcgtgt agtcgttggt aagctgaccg acactcctat acgggaaaag 180 aggetaegtt eegaggttat teettggaae geageetett tegttagaaa aggaaeetaa 240 teggaaggaa agagcataag gaggggttat aaacteggee tategeteat eagataatga 300 gaccaattcg agggacgctt ggtaacggct gccaccaata cacgatcttg gccgcaaagg 360 cttctgccaa tggctcggcc gcagcttgta cctagccccg gtagtcagca catcgtccac 420 caaaagaaca cggataccgg cacgcgcgta ttcggggaga gggcaaactt ccctttcatg 480 gctgactttc ttccgaatag gactgtccgg tctgactgtc cgtatatacc tttctgcgca 540 acettettga acaggtatte eegttaegeg aettaateet tgtgegatag gagtgeetga 600 ttgtagccac gcttacgttg tttgcgtggg tgtaaagaac cggcactatc agatcgtaat 660 cettggacag gaaaggatag gateggegge cattegteeg ageatttege egateteact 720 gtatcctcca tatttagtgc gtgtatcata ggccttacac ccccgtcctc tttgaaaata 780 aaaagctgta cagcgcgtcg atataaacat ccccattcag acgatctaat ccaattgcat 840 cccttcgata taccgnggca ttctcaccat gcaacgagga caaccccgat ctccgtctcg 900 gcgagcaagc t 911

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1582 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

```
ctcgatgaat tggtgctccc gtagtaatca tgacgatcgc ttggcaaccc aaaaaqcgtt
                                                                        60
taatetteaa etgaacagge gatgateeat acegacaagt gaccetgaeg ggaetateta
                                                                       120
ccggataccg aagcaagaaa cggagcgatc gtatcgaagc taatcgacct ttccatgctt
                                                                       180
aatggcgaac tggtaagctg atgggtccga acggctgcgg caaatccacg ctcatgcaca
                                                                       240
ccatccagga ttactgccac ctatttcgqq qaatatcacc atcgcaggac qcgaacacac
                                                                       300
ggtctccgca tgagagagaa agccaagatg ctcagtctgg tacgaccgac aaaatagcag
                                                                       360
cgacgaatct gactgttcgg gatattgtcg tctcgqacgc tatccctacg tcaattatcq
                                                                       420
gggtagcctg accgcaaagg aaaggagatt gtgaatgaat cgctcatagc atgccgactg
                                                                       480
atgggattcg atcgcgccaa tacggggaat taagcgatgg agaaaaacag cgtgtaatgt
                                                                       540
agecegeget ttageceaac agaeteeegt gatgettett gaegaaceae ggeacacete
                                                                       600
gacctgccaa gccgtctgga ggtgatcatc atgctgccga attggcacgc aaaacgaaca
                                                                       660
agagtateet egittetaee eaegaatgga tetggeeetg eaatgggegg acaeggtatg
                                                                       720
gctgatgaac agccagggga gatttgtcgt ggggcaccgg aggatttggt actgaaccac
                                                                       780
tgtttgaaaa agtattcggc aacgaaactc tttccttcaa tatagacagc ggaccttctc
                                                                      840
cgtcaaacat aaaacggcta cacctgtttc tgtagaagga caggtgctgc ctacaaatgg
                                                                       900
acactgagtg ctttgcaccg gaatqqctat qqqaatctqc aqatqcctcc qaccqcaaaa
                                                                      960
teaccgtggg agagggetge ggattetgea ggagggegat teetegaaaa gettegaete
                                                                      1020
categgetet tgetacaaac getgeaeget caccacgaat gaatgettgt gaaacaaaaa
                                                                      1080
ttatatgcaa aaccctacga tagatttcga caaagaaacg cctctgtttt tagtcctatg
                                                                      1140
ggcgatcctc tttaccactt gaaagaaagt atgatcttcg cttcgcagga cgcagaggag
                                                                      1200
tegtgageae etgeaatete aacggggeta eegagaagae eteegetaeg eetteaacaa
                                                                     1260
cagttgcggg agggccccga cgtaatagcc aaacgctctg tagggatgcg aggaaagacc
                                                                     1320
atgtcgaaca ctacgccgct tagcggaaga attgggtctg cctcttgaca aacaacgggc
                                                                     1380
atgggtaccg ctgctctgat cgaaaatacg gcgacctcct ccgccaatac cacggagtaa
                                                                     1440
cggtcatggc ggttgccacg gcaggtatag tgtaaatggg ggacgcgcag gagaacctgc
                                                                     1500
cgcatacaac gaatttacca aacagacctg attaaqccgg gtaccatcaa cgtattcctg
                                                                     1560
ttcatcgage ctcattggat gc
                                                                     1582
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 901 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION $1...9\overline{01}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

aaacgtatcc	tcatagcctg	cccctccttc	gtgtgcgact	gtctggagac	ctcgaagaag	60
tagccgatca	cggacaaagc	attttcaaaa	aagcaggagt	gcggatttca	cttacatccc	120
ctgtctcaat	agcggggcga	attggatgat	gctctccgaa	acattttaga	ggaataatac	180
agcatgctca -	gttatctacc	gatataccga	cagacctgcc	cctcctgagg	caagccgtcg	240
aagcctccgc	cgggaagaat	ccggcggtgc	cgtacccgac	tccgatcggc	cgaggtgata	300
tacgaggcgc	gcaaccggct	ttacgccatc	cgtaccgcac	aggagagcag	gtggtgaaga	360
gcttccggat	ccctattgcc	attcagcgcg	tgtctactca	ttcttccgcc	cctcgaaggc	420

tgctcgctct tatcgcaac	g catacggctg	gggcgatgcg	gcatcggcac	tccgcgaccg	480
tcgggctatg catcgaacg					540
catgcacgac tgtcgggat					. 600
ctccgtgcgc tggccggat					660
tategeeggg caacgtact					720
agacctgaac cggataagt					780
tttgacgtct gagcttttg					840
acagggettg aataeggae					900
C					901

- (2) INFORMATION FOR SEQ ID NO:102
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 664 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...664
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

aaaaaatctg atcatacgcg ttgcagacaa tggcatagga atagataaac tgatcaggct 60 catatetteg acatetteta tegaggacag teegetacga aaageatgga teaggegteg 120 gactotogtt taccaatata otggtogaaa oottogaggt acgatoaaag tggaaagooa 180 gccggggaaa ggaagtcctt caccatcagt attcctacac aaaaccagtc ctcttcggca 240 300 gagatettee ttggetacee teeteegatg acattgteat geetgteeae ateggeeega 360 tgactcaccg acatctccga tggtagcagc tctgaatcat cgctcgagga cgaacgtccg 420 accatactgc tcgtcgagga caataaggat ataacctgct cgtcaaacta ctcctttgcg 480 atogotacaa tgtgotatoo gogoaaacgg aaaagagggt atagocotog ctacogagoa 540 tattcccgac ttatcattac ggatattatg atgccgataa tggatgggat agaaatgaca tccggatgaa gcaatcgcct ctgctctgtc acattcccat tgtcgcttga cggccaagag 600 660 taccgaacag gacagattgg aaggaatcaa aagcggttag tetettatet atgcagecat 664 tctc

- (2) INFORMATION FOR SEQ ID NO:103
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 424 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...424
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

cattgcaata	cggactatga	acggctgcgc	caagcccgat	tcctcgcctt	catcatcatg	60
tctatgtagt	cctgaaagga	gcattcagtg	caacctgttg	cccggcggca	tggtcgtatt	120
caacaatacg	ggcaaccccg	gcatggcaca	ggaggaagcg	gcgatgtcct	catgggcatc	180
attaccggcc	tattgggtca	ggctatcttc	ctgcttcagc	ctgtgtcctc	ggcaattata	240
tccacgtttg	gccggagaca	tctatgccgg	acgctatagt	caggagagtc	tgatgcatcg	300
gatattatcg	acaatctggg	tacagcgttc	agacaagttc	gcgttaggac	ggaaatcggt	360
cnaaaaaaca	cttgatatna	gaangaactc	tttttttgtt	ccnaaaccgc	atcncttgtg	420
agaa						424

- (2) INFORMATION FOR SEQ ID NO:104
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 695 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...695
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

cggcgagaga	aatactgttc	ggagacgtcg	atgcggagct	ttacgggagt	atctgttcta	60
ccacatagat	aggtttcgtg	ggagaagcca	tatcgccgta	tcataattgc	gtgcggtaat	120
cacaccggat	atagggcttc	ggagcacgtg	ttctccagca	gattgttgta	agtagtctcg	180
gccacgtcga	gctgcgtttg	agegeatece	actgctgttt	ggctatgcca	cctattttgt	240
acagccatcc	atacgctgga	aattggtgcg	cgtattctcc	agttgtactt	tggctgggtc	300
agttggctcc	gatccaactc	ggcgagcacc	tgtccgcgtc	ccatcgatca	cctacttcgg	360
ccgtaaggcg	tacgattcta	ttgcccatct	gagggtaatg	ttgttggtca	cttcggcccg	420
aacggtagct	gtgaaactca	gacctcattc	agcgtgtcgg	tcttcactat	agtcgtctcc	480
accaatttgg	tgccatagct	gccgaatcag	cagcagacgg	ccggctctct	ttcttgccat	540
gcagctcgtg	agaatgagga	acggcaggac	tatgaggagg	atagcactcc	cagtgtattc	600
gatcttttca	tatttatcat	acaggtgtat	tttggtatat	ttacttttta	cgctcattgt	660
tcgggaatcc	ccatgccggt	catcttgcca	attcg			695

- (2) INFORMATION FOR SEQ ID NO:105
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 694 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...694
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

geetgeacgt	caactctaga	aastasst.				
	ogue ce caga	ggateeeeta	greegettet	ttgcgattac	tgtttcaatc	60
regulatere	cgcacagete	cagaaagtaa	tgtgtactta	gcatectett	cataaaaaca	120
atgactcaac	ggaagaacgc	ttcggatatt	t++00+~~~		cucududgea	120
totopatant		ceggaratt	cccaacgeeg	gtgttaagaa	acaaaacaga	180
ccccaacaac	cactgatgta	ctgtacgatg	acaaaggtgc	gatatattct	tacaaccett	240
ttccttgcct	cgcttnggtg	tacccataca	caggtttctt	tasatatasa		
atataacast	7,7,7		caggeeeee	ccaccycaca	agctctgcga	300
gegeggegae	gggagaacaa	ttcagagtga	gttttaccct	caagatgcta	atggaacgga	360
attcaaagct	cctgccatga	gcgactttga	agcctttttg	acccaaccaa	taataaaa	
teatteagtt	ccatttccaa	20222		geeeggeeae	cyclacaage	420
	ccatttccaa	Cycaagacca	ctttgtctcg	aagtatcact	tatacatata	480
ccctgatgcc	aaatcggtcg	gcacctttca	gateggteeg	gestesates	ataccasaca	540
cgagattata	agaccaagca	agtatogata	22222		gegeedaege	340
202242-4	agaccaagca	ggcacccacc	aaygigette	cggccgataa	aaatcatcga	600
addatactaa	gretteetet	tcttcctcac	gagtegagee	gtagtttgtt	gtccgaacca	660
tcatcaataa	gaccaatgta	CGAGCAGAAG	cast	5 5 9	, jaacea	
	J	- Jaguagaag	cgac			694

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 870 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...870
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

tttgcagacc gacgcacctc gccgttgcaa	gcccccgcaa acgggagaag tatccctcg	actificting great	gaatcgaata cccctcggtc tcccccggga tagacgtttt	tttgggtacc agccgcgtgc aacgccggga	cataaacgac tttgccgcgg gggaggagcc cgtggccgtg tctaaccttt	60 120 180 240 300
gacgcacctc	acgggagaag	qccqaqaqcc	tecceagaa	ageegegtge	gggaggagcc	
googeegeaa	tateeeeteg	aaaaaacgtc	tagacgtttt	gcccgaaacg	tctaaccttt	
- Je ou gaaac	gcctagacgt	LECATECGGA	acqtctagac	atttecteca	aacatccaaa	360
-30000000	cygaggactt	yagggatgta	toggtatgag	tggtcatcaa	ataacaacaa	420
actaataata	ageaugetat	geectaaagt	atgtgatcaa	aaagtctgtc	gccaagatcg	480

gccccaaagc	ggacagacca	tctattatgc	ccagccggcg	gcacaagact	ctgtaacctc		540
cacageetet	gcaagcgaat	agccgaggag	teggetetga	cctccgccac	gtcaaaggca		600
tcctggaccg	cctcgtcaat	atcctcagcg	aggagetece	aacggcaaga	cggttcgcat	78	660
cggcgagctg	ggcagcttcc	gcctctgttc	ggttccaaac	aattggacga	ccccaagaat		720
ttctctgtag	atcagtccag	aagcacaggc	tegtetteat	cccctcggca	gagctcaaga		780
gcatcccgca	cgcggcaagc	teegeeeggg	gtcttcagcc	ctggccttcg	actcgacgtg		840
tggagccgaa	gcctaagaag	aaacccggac					870

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 571 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...571
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

cgctgtggct	ttcttgatga	agtcgccaaa	ggtgtccttt	gcagaacgat	acgactgaaa	60
gagcgatacg	agctgatgct	gcgcaatcga	atcggcacaa	ggccgaggac	tttatctacg	120
aacagaccaa	tggcagttta	catcgcccag	cagcagattt	acgctcaaca	ccatactcgt	180
cttttatgag	ccgggagcca	tacatgttcc	gagctgattc	gccaactgca	tcaggatgat	240
tggctcgtaa	tttggtagaa	tccaaacaac	taagtatttt	attcatatat	tccgttatgg	300
ataaaaatgc	atgggtggcc	ggtttgccga	ttttcccgat	ttctggaagt	aggaatcaat	360
agcgatagca	gtatcacaga	tcgacaactg	tagatatcaa	agcctcacca	acgatctatc	420
tgcttgataa	tcacggatat	gaattctaaa	agatgtacaa	ataggagtta	taaaagagta	480
tctgaaagag	aaaaagaata	ctctctgctt	acgaagtatt	tatgcattac	agggaaaaat	540
accggagaat	cttctttgca	gctctgcaga	t			571

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 714 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

ntecceggee caeategtee aaacgggeag cagecetteg ttttgeteac gaaagegacg 60 agactttctg ccatatcggc tgcacgttcg ggaaaaagat gttgtacaag gggtgggcag 120 ctcggtaggt gtcccagagc gagaaggact gtagtgtttg cgtgccgtct ttagcgtatg 180 gatetttttg teegetetet gtaacggeea tetgeatege tgaaaacegt egggeagage 240 agacttgata gagcgcggta tagaaaatag tgtccactcg gggcgatatt ccttttccgg 300 cactttenen agacagggea egtttgeeae ageagegatg ettegeaegg tageggtega 360 aatcgtggtg gggagettet ttegeeagat tgtageeget eeettttegt ceaegeeega 420 tagggcggtg gagatcgtca ggtgctgtcg gacttggcta ttaaaaacga aaggtgggct 480 acaaggeegt accaatgaat tgegtegtat egttattgge atattggggt acaetgtett 540 cgtgaactgc tctatcggaa gagaaaatct gctgcggaag aatatgcgtg atcccgtgcc 600 caaccgtccg agaagcgata accgcttatc gtgtggcgtc gatcagcttg cagacggctt 660 gtetgtegte etgteceaat teateggeta ttgagatega ggegaettea gtae 714

(2) INFORMATION FOR SEQ ID NO:109

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...681
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

caagcaaagc taagtcccaa tctcatcgtc gggagggtga cgaacatcat acgccaaaac 60 cctgacaagc gaggatgaag agatacatga ctatcagctc ggcaagaatc cgccattgat 120 cgggtaggag aggaagccat acagataacg tctataaagg tgccgatgag catgaatgcc 180 acggtttggg gtagcacttg cccaaaaggg cgatggacat actgccgccg gccgtctcca 240 tccatctcga gctgtcgatc tcttgatctc catggctatg ctacacactg tgacatgaag 300 atgagcagac ccagtacgcc gggtatcatg atattgctca ggtgatggag tagttgagcc 360 acggattgcc tatggggtgc gtgtcgataa cgtcggctgt agccagtcca tggcctggct 420 ttcggtggct cctcgggcat aagttgcgaa cgagcggctg caccggctac cagttcgctg 480 atcatcttgt gtccctgaag aggagcgagc cacccaccat ataggcatag ttggtataga 540 ggagagettg ggettgette tgtgegtagg catecegtgt cattecetgg gtatatagta 600 gtaaccgtat atctcgcctc gctgactgcc agccgagctt acgcacgctt tcgaactgtt 660 gaccatttgg gttgcttcca t 681

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

cgggcaccct gtccggcaat acgatagaag gcaatgtaga gcagatgggt tcagcctgcc 60 120 gcttacgcta caacgattcg aatccaaatt gcccggcata cagccttgcc ttcgaccgaa gaagagetta aggeactgge agetttgaca agggeaacta caaatacaag gtagaagaet 180 actttgccaa acccaagett cegettttca getaageeee aacggcaagt aceteteata 240 300 tcaagcgtgc catcgaagaa aaggacgaac tgatcaaagg ctaggatgga tcaacgacga 360 420 acqtctcttc tttqtcatqq acaaaqqaqq gatqagaact atcacctctt tgcttcgaat atcgacggca gcaatacccg catctcaccc cctttgacgg agtgaaggct tcgatcctca 480 540 acatgctcaa gagcagaagg actacatgat catatccatg aacaaaaaca atccgcagac 600 ttcqaacct acaaactqaa tgtagtaaca ggcgagctga cccagctcac gagaataagg atgcqqccaa ccccattcaa ggntacqagt tcgacaagac cgcgaactgc gtggattaca 660

- (2) INFORMATION FOR SEQ ID NO:111
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 608 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...608
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

cggcttcaat	gctcttcgac	aagctgtcga	ggacttcgac	tcagaagaac	caagcacaga	60
ccctaccagt	ggaacaacta	ttcacagacc	gagatacaaa	ccgagatgag	agcaaagctc	120
				gtgcgcgact		180
				gctggtcggc		240
				ctttaccctt		300
				ctagcacagg		360
				tacggataaa		420
				ccgagggaag		480

ategeacet aggtgeeggt ettateaatg acaettacaa ggtggeaaca geegaageea 540 tgeacetgae taegttttge aacgaateaa teacaecata tteaaagagt ggaaatgeta 600 caggeeaa 608

- (2) INFORMATION FOR SEQ ID NO:112
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 655 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...655
 - (xi) SEQUENCE DESCRIPTION: SEO ID NO:112

tggccgttgc tcgacatgga aataagagag ctttgctgta tgctacatag gtgttctatt 60 tggtacgatg tacggggata ggctttgatt ttttccgtag tttgtattga tattgtttct 120 tgcatacaca ttcaaaacta ttgacagatg gcaagcgaaa gaaaactgaa aaagcagata 180 accggagcca tttccgagtc tttactgatg cattcctgct caaactcttt gtgaaagagg 240 aaaaaacgca gaggtggaaa ctatcctcaa tcgtattctc caacttcaag atacaccatt 300 gccaagatte gttgcaacga eggtaagcae aateetgcae tegaaagaaa tattategee 360 ggctcgtgga tgatttcaag gaagagctgt ccagatcgtg aagagtattt cggcgtgtgc 420 gtctgataat tgatttgtca ctacgtgcat taagcagaaa tagcgtaaca tatagaggtg 480 ttttgaagtt ttctcacgat tgttgctcag gatgatgggc tggaaagccc tcgtcccatt 540 gcaaatccgc tccaaagcgt cattgcgtgg ctcctcatac cagcaattcg actttttgct 600 gggcaaactc tactattggt ctatcggtcg gaaagccctt tctgatgaaa aaagg 655

- (2) INFORMATION FOR SEQ ID NO:113
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 562 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

aagtgatccg	agggcttctc	atatcctttg	gcatactgtg	agaggaaagg	aaaagcgcac		60
ricegracea	atgtttgeeg	atctcatagc	cageetteta	aagagttcga	tettatetae	76	120
actitigite	cacttgttgg	ctgttgttag	gtcagaccga	agtetataca	caaaccatta		180
ceccaaetee	acttatttt	caggtaagtt	ggcatctatq	ttcaaataga	ggttacctgc		240
caceggtttt	ctccaccggc	agcccagttg	gtcagagaag	tetgagagge	atttatccaa		300
ceacacettt	tatagtccag	teetttttgg	gagtgtcaga	tacatattta	ettettatac		360
gttegeaagg	gtgaacagca	agccacccat	tgcagaaaaa	caatcagtcc	gtttcatctg		420
accepted	CCCCCCCaa	atgaaaacaa	gaaagccgca	caagaatcat	cgatgcttgc		480
tactatassa	aaaggragge	ccaataggat	tcgaacctat	gaccctctgc	ttgtaggcaa		540
tgctctaaac	cagetgaget	at					562

(2) INFORMATION FOR SEQ ID NO:114

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{1}57$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

```
ccccgcggcg tcggccttga caatggctct gcaacaacag tggcactcga aaagctctac
                                                                        60
tteetgeteg aagagetgge tegeeeegae attacagega etategegee egeetgetgg
                                                                       120
toggagtogt totcaccott ogttocttoc coaccataco ogactotatt ataatgagat
                                                                       180
cgcattgcga ctggaaccgt caatgaacat atccetttgg aaccgaecet tgagatgett
                                                                       240
togatogttt cototttgcc tgcgaaacag agtocatcac caagcatttg caaacgagan
                                                                       300
cttttaagcg atatacagaa gatagccccc gacctgcgca aatcggtatg ggagataccg
                                                                       360
agtccataca ggagacaggc aatccggagt ggtggaggag ctggagaaga gcggtctggg
                                                                       420
agacaaaatc agggagttct cgagttgcag ctcgaaggag ccgatgtaat gcactcttcg
                                                                       480
ttcatgaact gaagggaagc agctttttcc gcgagatgca caactggttt ctgcctttca
                                                                       540
tgccgcccac agccggatag ctccactgct cgaagagaat gctgtgctaa gcagcttgtg
                                                                       600
gaggegatag geecacaget ttgeaacteg gaeegetete ttteategtt tegatggaaa
                                                                       660
gcctccctgc tgcacttcga ggttcgccat gggagccgta ggcggtgaac tggatgcact
                                                                       720
caaagagcag ataaacagga tgtaccggtc ggcgaaaccg gcaaattgga cacggccatc
                                                                       780
aagactatct gcaggatctg tacagattct ataaggtatg cgaacggaag aacaatttga
                                                                       840
cgatatttte etetegeeca teecacegga tetgeetgtg etgategeta tetetacaag
                                                                       900
cgtgatacgc tgctgcatac ggccgaattt ccttccgccg caagcattac gatcgggcag
                                                                       960
cgaagettge tggccgattt getgaaggga aagaaagtge caeggataee aetetgeaee
                                                                      1020
anagetgggt ttetecetee ageageaggg cettttegee caagetttgg etgeaatteg
                                                                      1080
cgtgccgact ggatcgatac ggagaacgaa tggctgctca agcgtatgct cactgtaccg
                                                                     1140
cagctgtgcc cgtccgg
                                                                     1157
```

(2) INFORMATION FOR SEQ ID NO:115

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH. 782 base pairs (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...782
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115

atgtacaag	gaacaaaaa	ctcgctcccg	atgagtataa	gatatggcgg	actccgtccg	60
ccgcagtat	t geegaattgg	gaactcctat	tgcatacgcc	aaacqttcaa	tatateatat	120
acguigeeg	a ctgcccaaat	atccgcatga	attgggtgaa	tggttcattg	acttataatg	180
ccgtgtata	a ttgggacgtg	gagcgaaaac	gactaccgaa	caaatcattq	ggaacacgat	240
ccggatcag	, caacgctgga	acttcccctg	caactcaatc	tgacatcgct	gtatgcaaat	300
ctgctttcct	: caagagaata	gagcagcaca	tcacgaatcc	ggaaaaaagg	atcctgtaaa	360
aaaagcagco	: cagccattga	ccaagaaaat	ccgttgctcc	ccgattccac	ggtaacactg	420
acgcacactt	ttgcgtccaa	gaagtgagag	tgtccgctct	cggtccggat	ggcaagatgt	480
atccgctgaa	acaaaaatca	aggacaagaa	tacaatcgtc	attttaaata	atgacagcaa	540
gagatcaat	i taacggtaac	teceeegagg	cagaacggct	ccactcctca	ttcggtgcga	600
taggcgaaag	gatggtatac	gccttgatga	tgctcaaagc	atcaacctta	actaccaaca	660
ategteegge	ttgcatctgc	ccggatcttg	cccaacatca	aagctgcagg	cqqacaaqqc	720
teegtggatg	gtgtttggca	ccgggatggg	actttgcttt	cggtcttacg	ggagaagatt	780
tc				-		782

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...4\overline{3}5$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

tececettg tttgggaagt	tcagactcaa	tagcagatcg	acgacctcgc	tccccttgtc	60
gtatttgaag catcatttct	tataatagaa	agaagacagt	gaagatggtg	atgatgtcat	120
ttttcagtac acatcgcctt	ttctttactt	tgtagagcat	ggtttcgaat	ttgggaccgg	180

cttttgaaat cagatnttet aagaaacgtt teaaagaact atgttatteg aategattae 240 ceetggeaat ggtggetgat ageaggtate etgetetttg tttttgagat tttteeegg 300 gtttettett ggettgttte ggtatgggag ettttgetge eatataeegg eggnetgggg 360 gttgtetatt gtgtggeaga eegtntttt taegtggett egetgetete getetteetg 420 eteagaactt ttatg

(2) INFORMATION FOR SEQ ID NO:117

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...601
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

60 ccggcacctt tcaggagaat accgaggata aaggcgagga taccgaacga gcaaaaacca geategeeaa agtatagtte tteggttege eggetgeaea eeettatteg tggtgtegag 120 gatggctccg atcacgatgg gaacaacatc aagccgatat tctgaataaa gaaaatggcc 180 gaataagccg agccaatact ttggggtcga taatcttggg gtaccgacgg ccagagagca 240 gcaggaccaa agagaaagaa atacccagta cgacgatggc tgcaatggct atggaagaga 300 360 agaagtggtg ccgctctcaa aggggaaaat ggcgaatgtc aggggcagat aaacatcagt 420 actgctccga caataagcat ggtggctcct ttccgacttt atccaagaat gcgccgagga 480 aaggogtcag caccatggot ccaaggggaa catactgaag atacgggcag ctccttcggc cgtcagaccg tatttggact gaagcatctt cggtggcaaa acttcttgaa aggggaaaag 540 600 gettgaatag taaageaege acaggaggge aacattecag acatgetatg cegaaceetg 601

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 594 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

ccgttcaaca cataagtccg tttgtcggat gcgggggctt gccaagtgag gtcactgtct 60 120 geoeggatac agaccattgg agattetgta egggagegat teattgeeac etteteeggt cactacaacg gacgcagcat cgccgggcct tgtcgttgga cagtgaaatg ataagtctta 180 240 coggoctota coacatatog ttacctttgg agacaccoto tootactata tatattatgo 300 caggatgggg ttaatgatta catagtcata agtgccggca ggaatatcgg ctgagctgtt 360 ccatcaagca cgaaattcgt gggagaaaaa gatgcatcgg catgaccgga actttatact 420 cgaaaggatc gtaaagaccg gccgggatcg ttcgttggca aaccaaaaag attcttcggg aatggatgcg ccgtactgat ttgatctgca tcccagagca tttgatagcc tgtgccgtct 480 540 toccatacat gtgagoctoc aagataatto gtgocataco ggcaggaato ggatotoggg atcettggcc ttggatgttc gaatacettt ctgcaccgct tgggtgcgca caga 594

(2) INFORMATION FOR SEQ ID NO:119

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 830 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...830
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

ccctggctaa	tgtctatccg	atcaatagct	tcgacggtat	ggctaccgaa	gtctcggacg	60
ctttcgtttt	acgacgagca	gcactttccc	gatgcgtccg	tggtttcgca	tatcaattat	120
cactccgata	cgcttaccat	tcggaaggag	atccgatgga	gaacatccgc	atccgcctgc	180
gcgagaccga	tgactaaagc	tctccgaagt	cgtcgtcagt	gtctccgctt	teggggtggg	240
aggcagcaga	acaagacggt	gctcaatcct	atggatgtct	acacgaatcc	aagtgtaacg	300
gagatctctc	gatggcgctg	cgtcagacac	ccggcctgca	ggagtgggag	atcgtgaggg	360
ctttttcgtt	cgcggaggag	cctcttggga	aaggccgtga	cgatagaagg	cattagagtg	420
aagcgttttt	tcggcaagaa	cgattcgacg	ctcctgctcg	ttcacgtttc	gagacaggaa	480
tgttcagcgg	ctttcgctct	ccaccggagg	ctatggggcc	acggaaggcg	gtgcgctgac	540
ggactactcc	ggttgcgatt	ggcgggtaag	tetecetegt	ccgtcgggta	ggaatatccc	600
cgctttttgt	aaacggtggg	ggtgggcatc	tttccagtcg	aatcgtttct	atatagagca	660
aaatgcctca	gtgagcgatg	ccgccttatc	cgtctgctgc	tcaagcccgg	agtacaaact	720
gcccggtacc	aaccgtccta	tgcctacaat	gcacggacga	tatggaaccc	gacttcgcaa	780
gatgagtgaa	ggggcttttt	ctcttcgtac	acgacctttc	ctctttggct		830

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...355
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

cggaacgatc	cgatcgaaac	cccttttttg	cgatagagac	aaataagacc	aggtatgaaa	60
cgattgatta	tcgcaggcgt	tttggcatgc	gccttgtgcc	ggtatatgga	cagagagtac	120
tgagcgtgaa	cgaatgccgg	cgccttgcct	cgaacacaac	agagacttgg	ccataagccg	180
cgaaaagata	aatgcgccac	cagtactcgc	aaagccgctt	tcaccagcta	cctgcccgag	240
ctctcgccac	cggtacttac	ctgcacaacc	agaaggaagc	tatcgctatt	gagcacgagc	300
agaagcacaa	gctccagaat	ctcggtaccg	accttgtcac	agcatagggc	agaat	355

- (2) INFORMATION FOR SEQ ID NO:121
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...642
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

cggctcgtgc	aggacaatac	atgettgtet	gtacgggcga	tatggaatcc	ttatqqaaqa	60
tgcctcatgg	atagagttgg	cttccataga	agtagcaggc	atacgagcac	ccattcatcg	120
ttactggtgg	cctccaaccc	acagatcatc	ttctcacagt	tcatcgggcc	aatcccgaga	180
cattgccgac	tttcagatta	caaatgaagg	tggtgctact	ttctccggga	aaatcgaaat	240
agtggtataa	aggctttctc	ggaaactttc	ttccaagcga	aagaagaaca	catggteteg	300
cccaagggga	aaccaaagta	ttgtctccgg	agctgactgc	gaatcttctc	tctatacaaa	360
tgccgaactc	tttcccgatg	gcacctatta	catgtcatca	gagagcaggg	attttgggat	420
ccgatcgatt	tgtttgggga	cattactatc	gtatccgtct	cattacggat	ctatcctctt	480
cggacatcgc	ggtaaggatg	tttctactat	agtactttat	cccaatcctg	ctcacgactt	540
gtccatgtag	ccattcctcc	cacatatgcg	ggcagcacac	ttcgtttgtc	gatattcaag	600
ggcgaatgca	gctctccacg	aagatcgaat	ctgccgaatg	cg	-	642

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...398
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

cgcttcggtc	tegeceggat	atgctccctg	ccactgagga	ttgtcggaac	aagcatcgtg	60
			ctgtcgtatc			120
			tgtctgcttg			180
			ttttgtgcct			240
			gttcggttca			300
			cgctgtagct			360
		ggttatccgg				398

- (2) INFORMATION FOR SEQ ID NO:123
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 644 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...644
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

atccccgaca aaagattttg	aaaaaatttt	ttccgaccgg	ctgatcgaga	ctttcttatg	60
cttccttgcc gatggaaaaa					120
gtacagetgg catatagage			and the second s		180
atatogtgat agaaacttog	aatatcaagg	tctcgtccaa	agcgttcttc	acccccgtat	240
togottgotg caatgoatag					300
gggccagagt ttgccgttct					360
attgatagaa ccattggttc	acttctgctc	caacaatgcg	aatacgtcga	ttggcgaaaa	420
tegetteata etecteegee	aattatgcaa	tagctcattc	acatctatgc	tttcctcctc	480
agggaattga ggttttcgat	tttgctatag	aggaggaggg	ttttattgag	ctgtacaatt	540

ggttgatgga ctgtatagcc ttataaatct gttcgagctg ctgtcattaa aggagggatc ttgcagtagc atttccagtt tattgcggct tatggccgag gtgt	600 644
(2) INFORMATION FOR SEQ ID NO:124	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 307 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1307</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124	
ctttgaaggt cccctctaga ggatccccgg gctgttcgct ttcttttggt cgggccgatt tgaggactga ataggaaata aatgttttat aagacaaaca ataagatgca gatgagaaca tttcgtgtcg ttgcgatcgt ttcgctgtct tttcttcttg gatgacgctt acggcgcaaa agaatagttg gtgggtggtg cccatgccgg acgcgagtac ttcaacaaca caagtgagga tatgagaaag gatggaatac cggagtagtc ctgcgctact atttctccga tcgatatatt ctttggc	60 120 180 240 300 307
(2) INFORMATION FOR SEQ ID NO:125	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 654 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1654</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125	
cggcagaaat aggaaaaaag gaacggatge atgtcagact ccggttggag agcttaagct cggagtccgg acctacatge tggcagaacg tcttttccg ataagctccc cactcaaatg cgccacttgg gtgctatcga tattatgcag ccgctaacgg ccggctggac gatctgcgcc tgaaaactcg tgtggaacgg atgccggage tttgaccata cagggcagca tcggcctcga	60 120 180 240

```
tteteetgge gaettgeega tgtagatget catgegaeta eegaaagaet ggaateaage 300 teatggeaga eeggeaegat tggeetgaae atgtggegtt egaetgaaga tgaaggeeeg 360 aetggetgee ggeaatetee tetegggaag tgggagggae gegtgtegea eetgaettte eegaggaetata eetatgagga etgaeegateg aettaeagge egaeaagggg eagtgetag eetttetett egagttette eeggttegaa tggaatetga eagegeaea ettegteeg aetgaeettt geeegettegaa tggaatetga eagegeaeaa ettegteeeg aetgaeettte eeggttegaa eeggeatete teetgatte tee 654
```

- (2) INFORMATION FOR SEQ ID NO:126
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 646 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...646
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126

cqtattcaga	gcgatatgct	gctttctact	gcccaaaagt	ccaagaacac	tggttcggca	60
			attatctgag			120
			gagatggggc			180
gtgaagggaa	gctatcttgg	gcggagctga	ctatgggaga	cttctacgat	cagttcggta	240
			caacctcggt			300
			gtgcgtgtca			360
			tcattccggc			420
			agtgccatgc			480
			aagcagacga			540
			caatgtcccg			600
			gagtatgata			646

- (2) INFORMATION FOR SEQ ID NO:127
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1231
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

gcgactttcg gctcgtattt ttccctgatc gactgaatga ctctgcgcct gatgccgttt 60 ttcttctatt tgtatcggtt gttcttgcca taggcatgca ttgaacttta atcattattt 120 tegeacegga etttgattae agtgtaatat gaaaagaata gtattgatte geeacggega 180 aagettgtgg aacaagaaaa tegetttaeg ggatggacag atgtggattt gteegaaaaa 240 ggtatgaaga agccaagaaa gccggcgagc tcatgaagaa agaaggcttt cagttaccaa 300 agectatact tectatetea aacgtgeegt caagaceetg aacgtgteet egatgtaatg 360 gacttggatt ggataccggt ggagaagacc tgcgtctgaa cgagaagcac tacggcatgc 420 tgcaaggcct caacaaggcc ggactgccga gaagtacgga gacgaacagg tactcatctg 480 gegtegeage acgaegtece ceceaegeet atggagaaag aggateegeg eteteegtta 540 tggatccgcg ctacaaaggt gtgtgcgaga aagacctgcc actgacagag ctctntgcga 600 cacggtaaat cgtatcctcc cctattggaa cgagacctat tcccccacgc tcaaggagca 660 tgacgaggta ttggtagcag ctcacgcaac agtctgcgtg gtatcatcaa ggtgctgaaa 720 aacatttcgg acgaaacatc atcagectga accteeegae ageegtgeet taegtttttg 780 aattgacgac aatctccgtc tggtgaagga ctatttcctc ggcgatccag aaggatcaaa 840 aagctgatgg aggcagtagc caatcagggc aagaagaaat aacccccatc gccggccctt 900 tectattetg ettttegaca gaaggeaagg aaaaaaacaa gaagagageg ttgeacgace 960 gttageggtg caacgetete ttteatttea tetttttttg eteggttgee geagatgtta 1020 tttgeteega ggtetttete etacaagace ttgtegtaca catgeateag ggategggta 1080 cggcttcggg tgagaaacgc tctatatagg tacgcccgtc ggctatctct tctcgcggag 1140 agagetgteg gagaggatge tgtecageat ggatgeatea ttteegeate gteggggteg 1200 gtgtacaggg acgaagggcc tccggttctt c 1231

(2) INFORMATION FOR SEQ ID NO:128

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 598 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...598
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128

cgatttetgg agggetatea teegateeag aegggatage tttacetete gggeacateg 60 teegegaggt ggegageage ataagtacee ggeegttega atacttgaac atgaaggeag 120 agtogtaacg cacctottoc atcaggogag agtggottog aagtottoot cogtotooga 180 atggaageca cagaagggte getgetgatg gegeagteeg gtatggeeeg geggataget 240 gctacctgtc gagataccac cggcgcgtat agccgcgctt catgacgcgg agcacttgtc 300 getteegete tgtgeeggea ggtgtatatg attgeagata ttgggtateg tgeeatgaeg 360 gcgatggcct cgtcatccat atccttgggg tgggagaggt gaagcgtatg cgcatgtcgg 420 gcacagette ggccactget ggagcagate ggggaagegg atgateegee egttttgtte 480 gtatcggtag agtttacatt ctgccccagc agcgttacct cgcggaaatt cttggcttta 540 gatecegeae ttegttgang atgettteta tttegegget tetttetege etegtgtg 598

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1412
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129

tttcgtagcc atgcacttag tgcggacgaa tgagagagag atcttcttgt ccgtgtaata 60 gatacccgtt ctatactgag agccgacatc gttccccttc tattgaggat tgtaggatct 120 atggtcttga agaaaagatc gagcagcgag agagcgatag ctcactcgga tcatattcga 180 ctcttaccgt ctcggcaatc ctgtggtttg ggaacagacc tcttcatacg aaggatcctc 240 gacatgccgt tggcataccc gacttcggta gccacgacac cacgcacttg tttgagaaat 300 gctcggtacc ccagaagcac ccaccggcaa agtatattgt cttgtctcgg gaatactgtc 360 attatgottt googaagaag agcaactaco ggactaagag aaaaactaaa agaagocata 420 ctgataagaa taagagaaag aacttcataa caaatcggat tctcttttca tgagaatggg 480 gaagagacag ctcgaagtag tggcaggtcc tattcatgat gatagggctc atggttgaga 540 tagtcatggc acgatacacc tgttcggtga agaagaggcg gatcatctat gagagaaagt 600 catteggetg agegatatte tateggttae agecteegea etgeaggget aaateeatat 660 gggcctccta tgacaaagac cattcgcggg tgccgatcag cattttcttc tgcaaaaagg 720 ctgaaaactc catgoggaat actototgoc togotoatog agcaatacgg tgotqtooga 780 cggcgaagac gagcgagtat ctcccgacct tcggcatcct tttgctgttc ggagaaagct 840 tgctacccag acggacatcg ggtattacct ccacttcgaa agaacataat ggctcaaccg 900 acgaatgtat tecteegttg cetgaaceat tgtttgetgt eggtettgee tacaacgage 960 agtacgatct tcatcagaaa gcagatcatc ccccgcatcg gcgttggaag cccaacccgt 1020 tgccggctgg acggcatgct cggttgttgc gttggaaaag tcggagcacc ggcggcagca 1080 tttcctgtgg caactgctgc tgaccttgct ggcccgatat atccgcgtcc atgcgccaag 1140 ccttcacatc ggtgtaccaa cggccgttga actcacgctt tcaatatcga cccagaccgt 1200 aacctgatcg cctacttgat aggaagatca atacgatctc cccacacgct gaagtgtatt 1260 ttgcgagggt attgtcgagc gtttccagta tgtactcttg ttttttccat tcctttccgg 1320 aagettgeeg actecegaat tgagtggeag tatetgaata agetgeeett gatetgaata 1380 tccatatttg ttttgttcta acatagttat cg 1412

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 612 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...612
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130

cccggtggag	aaaatagaga	gaaagctgcc	atcagctgga	cggacgaaag	atgaagttag	60
tcaccgaagg	agaagaacag	atcttcaagc	tcatcaggaa	aagtaatccc	accacccccc	120
actatctctt	ccgttcggaa	tggaagcgat	aggaaaagag	gatatgctcc	atgcaccgag	180
tgccggcata	tcctcttct	ttttcagcta	ttgctgctga	tgaaacagcg	tcccccgtca	240
gtctacctgc	gagagccatc	gctgataacg	acattgtaca	ccttgggttc	gcggcgaatt	300
ggttccttgg	aatctctnct	nggcattctc	gacaaagaga	tcgacagttc	tttcttgacg	360
aggttgatcg	tacaaccgcc	aaatccgcca	ccatgacgcg	cgaaccggtc	acgccacaat	420
cccgtgctat	gccgttgagg	agtcgagctc	ttcgcagctc	acctcataga	gacgactcat	480
accatcgtgc	tttcgtatat	tttctgtcct	acggtttcgt	agtcgtcgcg	ctccagtgct	540
cgcacacatc	gagcactcgc	tgcacttctt	cgacgacata	ctcggcacca	tataatcctc	600
ggcagagact	te					612

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...509
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

cggaaatttc	tatttgctcg	gtgcccatat	accggaggtt	tgacctttcc	gaagacacta	60
agaatcagct	ctgcagcaaa	agagctcaat	caaactccat	gcaacagtct	cattttggaa	120
gattgccgaa	cttatagagt	cctaacagca	tatccttatc	gttcacttag	atgaaaggag	180
accgcagtaa	gaatattaga	actggaaata	tatgaagggc	tgtatttccg	agctgcgtac	240
ctgaagatga	tgaagatcag	gagaacgagc	atcagagttt	gcaagacgaa	cggacacgct	300
caagcatgga	ttgcgccctg	tttcgcttac	ccttaccgac	aaatgcaaca	ggtaacctat	360
gaccatcagt	acgacaacgc	ccttgtagcc	ggaatgaatt	ggaagaaaac	ttcgggatgg	420
aagtcgttga	atattngtcc	agaacctgtc	cggccaccgt	catcgaatcg	gatcggaaga	480
agatccaacc	aaacagacga	gatggaaag				509

(2) INFORMATION FOR SEQ ID NO:132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...664
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132

cgagctgaaa caaaccaaag tgacccagcc ggcgatcttc ctccactcgt gattctggcc 60 aagacgatgg gcgaagactt ccgtcccgat atggtggcgg ccattcgctc ggagagtttt 120 cggcattggt tgcagcaggt gccatgactt cgaagatggt cttcgtctcg tatcgaaacg 180 tgccatggcc atgcagaagc atgcgaagta cgcccctcga ctatggcggc tgtactgggt 240 ctgccgatga aaaggtggaa gaaatctgtg cccaagtgac cgatgaagtt gtcgaccggc 300 caactacaac tgcccgggac agatcgttat atccggttcg gtaaaggagt ggacagagct 360 tgcgaactgc tcaaggaagc cggagccaag cggctcttaa gctcgctgtc ggtggagcat 420 tccattcccc tctgatggaa cggctcgtga agagctggca aaagccatcg aggagactac 480 gatcagtcag cgatctgccc catctatcag aacgtaacgg cttctgccgt caccgatccg 540 cagagattaa aaagaacctg atagcacagc tgacggcacc ggttcgctga cacagagtgt 600 getgaatatg acaageeega tggtgeegae eaetttagga gttaggeeee eggaaatgta 660 ttgc 664

- (2) INFORMATION FOR SEQ ID NO:133
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 733 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...733
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133

agtegateag accetegega tegaaagege geaattette egeggeageg taegteeaa 60 geeengtaag tetgeaataa teggeeeace ttgageaget atggeeateg agatggegea 120 aggeeaagge cageegetet tegegageaa attgggeega eggggaeggg egtaeegtag ttegeaceag atgaaeegag taegageete gagaateaat geettgtegg ggeggaaatt 240 gaeaeteeta tegteaeget ggeggeatta eggegtgtge egeettegge eteeegggtt 300

ctacgccttt	gtgcaaggtg	agcgaagcgg	agaaagagcc	gattcctcta	tcttcaccgt		360
atatcccgaa	gccacgccgt	gggctatcgt	ccagccaagg	ccgtaaccaa	ccctttgact		420
tcacccgggg	agaatgtcga	tgggaggaaa	tcagatcggc	tatctcgtcc	agccccatcg	7%	480
tgcctcggct	atcattttcg	gatacatcgt	cegettgeee	gtgccttgca	tatcgggcat		540
tctctcatca	caaacttggc	catttcttct	gtacagctat	atcggtttct	catcgccggt		600
cgattgtttt	cttccgggcc	gggaaaattt	ttcccgaaac	cgacaaaaat	aaattttccg		660
gccggaaaat	ctctgtccga	anccttggat	atataaatna	aatctttgga	tatatgttcc		720
aaaactttgt	tta						733

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 738 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...738
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

ggccatatag accagaccac tgaggctgcg aatcaaaact gctttcatac gtaagctcga 60 tagtotottt atattttatt ogggatgtto ttoogtotot ottotocoto aacgggaatg 120 ggtgcttcgg catccgctgt tgtctctctg tggcggtagc cggtgcattc agcccaagca 180 attettetgt aegegageee caggggegtt tgeegaatat aegetetaeg teateageea 240 gaateetteg egettgagea acagatetge eagttegtgg tgeeeggett eatgtegege 300 agaatgettt tggegegete gtattgtteg gatattatte tgttaetteg geategataa 360 cctcggcggt agtatcactg tacggctttg tcgattccag ccgtcgtttt gcatttcgta 420 gtagttgatg ttgggcaget ttegeteatg ccataatagg taaccatgge gtaagccaac 480 ttegtaaege etecaagtea ttggetgeae eggtegatae aegteegagg aagagatete 540 ggcggcacgt ccacccaaaa gggcgcaaag ctgatcctgc agagcctcgt tgtcgtgatc 600 660 tgacgctctt ccggcagata ccaggcggca ccgagtgctt gcctcgcggt acgatagtga ctttgacgag aggattggca tagcgtgcat ccaactgata gtagcgtgtc cggcttcgtg 720 gatggcgatg ctgcgcgc 738

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 733 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...733
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

cggcattatt ttttttctga actatcattt tcttactatg ctgtatgctt atcgtatggc 60 tgcattttgc tgaggccata cgctaaaaac atttcaaagt atgtatttgt ttggataagc 120 180 ttttccctat catatattat cgctgctgtc taacctctat cattgagtat cgtatcatcc 240 gccagcaatt cggttaaagt teeegaeggt attetggtgg tagaaactte ttgteaggeg 300 gatagtgggg taagcctgaa cgtacaagaa aattatcatt tgtgggacca aaaacgtggc gcggcaattt tttgcttttg gttcgggaaa aaataatttc tcgaccaaaa cgaaaaaaa 360 ctcgcgcgta aattttcaaa aatacgaacc atatctcgac actttgggtt cgtaaaatct 420 480 ttttggccaa aatctttcgg aaaaacaagg taagcctcat catctttctt gttgtggaaa 540 teegtgtegg atggagtttt acaeeggttt teetgtegge etetteeate aataeegatg aagcaattcg cagggtctgc aagtttgaac cggatacttt atttttgtct cattacgaaa 600 ctattttcgg acagcgatat gagccaaaag cctacaacga tcggaaaatc atcctcatta 660 ccggcgggca cgttcgggca aaagtcctat gctgagcaga tggcactagc gcttgccgtc 720 733 atcctatcta cct

(2) INFORMATION FOR SEQ ID NO:136

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2287
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

ttcataggta taaacgaaga cagcacgacc teetttegtg eecategtag gtacacgata 60 tgttgcgctc catgcttccg cctcataagt cctttatgta caatactcca aggattttac 120 cgattggctc ccttattact ggcaaggtac tctcagacta cgcgatatac gtacaggata 180 gatctaagcc ctggaacgat gtcgtacgga tggctnattc gncccgacgc catgaagaag 240 300 atacgaagge tgaaagagae ggaeteeget gtacgtegge caeggtggae gaeegetgeg 360 cctctgccgt atatccatgt tccgacagga agcatangga tttgcagcgg agacattgca 420 gcggctggcg gaagtcgcca tcgaaaggca tgaggtgaaa tagtcggttg cgaagatagc gaagggegte tactggetge etetteeteg eccaegatea taacaeggee tacaegattg 480 cttccggcca attcgtgaag gacaggggcg caatgccgga gcttttgtcc tgtatgaggc 540 atttggaggg cttgtgagat ggaaggcatt catacatttg acttcgaagt tccatgttgg 600 660 aggggataga gggattette egetegtteg gaggtateaa acacettatt teegaetgte 720 caaaggtcgg attggcttat atggccacta agacgtaaat ggcgagcctt tcatgatacc ggtcagcaaa aacagtatga atactgaagt aatccactac atcattcgct ttctgatcgg 780 agataaagcg gaaacgatca gctcctcagt cgcatcggtt atacctcgaa gcaagcgaga 840 tgtcccgata cagcattgtc atccgtgctt caaacttctt cgttcggata tttacgtacc 900

```
gataaggett tteeettgtt acegetgaaa gatgggaggg egtaeetete etttttggag
                                                                       960
agecgacega agagetgttg aagagagega cacactggtg etgaatgeeg acattgtege
                                                                      1020
ctctacatat tctgatctcc cgctacgaag aggatgtacc ggcgtaaact tcgagataac
                                                                     .1080
acggacgatt teegggaaga gagteettge ettteaaage aggattttae agegteetgt
                                                                      1140
agtagatgaa tacggggcca ttctgcgcac caaaatcgtc agatgggctg gccggtaaaa
                                                                      1200
gacccagtcc cccatttctc catgggaatc tgacgcatga cgtagacgaa ccgttcgagt
                                                                      1260
acagaggatg gagagttttg cccgagcatt gatcaaagga acgcaaatct cccttcaagg
                                                                      1320
cttccgtctg gcttatgcca atccggcaag tgatcgtttc ttcacttttc ccgttttgtg
                                                                      1380
gattgggata aaatattgcg cagcaaaatg ccggattgct gcggattatc ttcttctca
                                                                      1440
aagcaccegg aaaggcccca caggatgcac gaactattcg ctgagaaaac cgctctatca
                                                                      1500
ategeteega tetttggtta aaacaatgga atagtgatag ggetteacag caactactet
                                                                      1560
geoggtetaa cecagaactg ateggaaage agegeaageg acttatgage gatacegtat
                                                                      1620
ggcagtcgac tgcaacaggc atcactacct tgcagctcgt gagccgagga catgcaagcc
                                                                      1680
ctgatetegg caggtateag acacgattat accatgggta tgeegatgtt geaggtttee
                                                                      1740
geettggtac atcccgtccc gttccttcat tatgccttcc acaagacggc tgaccgagct
                                                                      1800
gateetgeae ceattacaet gatggattgt aegetgeaea ggeaagagta tatgggeetg
                                                                      1860
gacgaagcta cggccataga agttggtgca aggaaactgc tgatgcatac ttcatccacg
                                                                      1920
gaggagaage cacacteett tggcacaacg aatatetete egenacatte ateeetggca
                                                                      1980
tgcccgtttg tatcgagaag tactgaggeg atagaaacca tggaggaaaa acaagaggag
                                                                      2040
gaatettteg actaegaacg geeategace aatgaaacgg gtaeteatet tegeegatat
                                                                      2100
etteeetegg ettttgetee gagagetgee tatetgacea aatatetgee tegattggtt
                                                                      2160
gggaacettt tgtaataacg gaaaaaatge egacteegge ateeegtege acggegatgt
                                                                      2220
gtttggtgga ttttgcagtg atattccggt aacgctatcg atctctcttc ggcttcgttt
                                                                      2280
ctgtctc
                                                                      2287
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 707 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...7\overline{07}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

ctgcgccaaa	agctttacgg	ccaataagcg	tettttegge	CGCGaCGaGC	gtataagcaa	60
acgagaggag	agataaaccc	gagaagcata	atggctgcac	agcctgcttt	getteggatt	120
cyccaeceet	ctcgctttat	ctatcgcgtt	tcttcggatc	agtttgcggt	ccggcttacc	180
aacceeerge	acatecetta	tacatcggca	gatecacacg	aagagceteg	geeteaegea	240
cyacaageeg	greagegret	ccacttccgt	ggatccgccc	tqcaaqaaat	cacttacact	300
acaaaaaaag	tactttcggg	aggcatcttc	cgctgtttgt	ccatagetgt	tagactacat	360
categgggae	tigecegtat	ttggcgcgga	aagctcggcc	acctcttcca	ataaagacag	420
cagetegggt	regrattegg	taaaatcgag	ccgatgggtt	tatcaaaata	aaccataaca	480
gragecycta	ggagaccatc	argaatttct	tcataatgta	ccaatcgata	teggteggat	540
acacgeaega	acacccgcag	cagtaagcag	ttcggcaagg	cgcacctctc	atecatetae	600
ccgggaagte	ccgaaccgaa	atagaaaagt	tcgcgatagc	cttcagcgtg	attaagccgg	660
gggcactctg	cgagcagaaa	tatagaacat	cctttccata	cgaccga		707

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 440 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...440
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

caggacgaac	caccgagtgg	agtgccacag	tgcttacgcc	gggtatttat	cccgttcgaa	60
dacddaacdc	aatcgtctgg	gaattaggga	gaactctcgg	atttgggcag	ccgagaggtg	120
atassassa	ctggcgaaat	cttttggatc	catecaaaqt	ggacgtttct	attcgtccgg	180
Ctyaaayaay	ccatgcgctg	222233422	agtcaagtca	tttagacaag	ttaataaata	240
gttggtttta	ceatgegety	ayyacaayaa	agtcaagcca	netateccat	ccasadacas	300
tttactccag	teegtaggtt	ataatteagt	acteetgete	aacycaccyc	ataataaa	360
ggcctgatcc	acgaagccga	tgccttgcgc	ctgaaggagt	gggtgactat	eccygecygy	420
cctttgctca	tgacagggta	gtggattttg	gccgctatgc	cgttgttcaa	ggacatgccg	
tcgaagaata	tgcactcgaa					440

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 787 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...787
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

226202324 Annual Republication of the Control of th	60
attgatatac aacaaagccc ttttgctcga attggagcgt cggctccgaa tgcccgcacc	100
attgccgaag ggtacgaagc gcgcctcaaa gccggtgaac caaccagttg gaatacaaca	120
tagatagaa tagatagaa tagatagaa tagatagaa	180
agatcaagct gaacctcgcc tccgtcgagg tgaaatatcc cgcgtgcagg tggatcgaaa	240
ggctctgctc gtccggtcga gcggttgaac ggaggcaaag agatcgcatt cgacgaaagc	240
cgctaacgga gatcgtgcta ccgcagtctt tctctgtatg gttcgatcag gtagggaaaa	300

aaaggtttca caaacaagcg tatacagcga ttatcgcaga ggagagatct	gggagtatet aagetteggt getteagete etgetgaega eettgetgga	tcggaatatc cagagccgca ctgtacgaac cctccgacaa ctatatgtcg	geggetatgt egtgeetetg gaaatgegtg gtgeegeegg tgeegaetge aaatgggaet	aagcgagaaa tgggaaaaca agacggacag gctaaagaca tcaagaaagc	ggtagcattg gtcgggagcg aaaaccgcgt tcggcagcac cggcggaaaa attggatgca accgtcagtc	ðs.	360 420 480 540 600 660 720 780
,							787

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 687 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{87}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 880 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...880
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141

60 ttacacacta aqatcttqqq aqttataqqt tqttccqttc aqqcaattqa tagqqqqcaa tectgettet geeggateg gaccaacatt gaaattegat tgettttnng accgaatgtt 120 quaqtucqua coggaagatg ggutatacac aagguagatg guggtattuc gtagaggata 180 240 acqqqctatc ccatacgctc ttcgagctan cgctgtagag ctcggcgagg tacgctctac 300 agcqtqcqaq ccqaqccqta qaqttccqct ccqtqaqccq tagatqtqqc cgagtqaqcc 360 qtaqqqccq qcqcqqtqaq ccctacaqcq taqcttgaag aqcgtagagc gcagctcggt acgetetacg gegtageeeg agtegetgta ggegtagete gaceeeettt eggegtatgt 420 tecquatqqc tataaaacaa teqqatteqa tetqaaqaaa atatqcaata tqetqtttqt 480 540 caqcqtattt atttctcggt tgagaaattt cagcttcgag aggcttcgac atccgatgaa 600 cqtcaaactt tttccctttc attttctqat tcqattatag tcaatatcca acaagagaga 660 gtcggcacca tatcgcttac atcgaactca cgtttgatag ccacttttcg aagaaagatt aggatctatt ctggcaaaag ctcttagctt tccgcgaaat agttttaact attcatcgaa 720 atggttctaa gtacttgtga aaagcttaca aagcttttca cagagtattt aatacttttg 780 tqtcatacct caaqaaqatq qaqqaataaa ccaatqcaqt tccggctttt ccggaaagct 840 880 taaggtattc acttgcacac cacttcttat tcttaatgcg

- (2) INFORMATION FOR SEQ ID NO:142
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...627
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142

tggattccgg cagatttctc cgtccaactt tagaagaatg agttggatat ttggggtaag 60 120 aggtgtagat ggattgttgg aaacataatt tgtagggaat taattgctcc ttgtataacc 180 aaatcaatgg gatcattcgc atttccattt tgccaatgaa gtctgcagta gttacatttt 240 gcagtgaagt ggccataatg tttctcgcca ttttaagccc cccctgggta tgtgtcccca 300 360 aataggagtc aaagcccgga ttttttgaca gagaaaagca gtgctttggt aaaatcagat 420 aagcgatgag gctcatggtc ataactcaca aggcgatncg caccccttct gtagccgtcc ccttaggcaa cattttttc aaaaacgctg tcccgatgca atggcagact ttaatctggc 480 aatgttttgc ctcccattga cgaagactgg tcgataacca tcaccacatc gacaggtacg 540 ttaccgcttt agtagtgatt tttagcgtca catcccaagc attgggattt caggatccat 600 tggattggca accggtaccg catactt 627

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 679 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...679
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143

ctgttgaacg aattgcgatg taccatgacg ggcagggtca gcttccatcg ctccacgcat 60 gcacgaagag categggcat atacatcata tecatatagt accetettta ateggacaag 120 tgaagegtee ttetttgaca getgeatata aatateeaeg geatagteeg tegtteeaee 180 accggggagg gtgacgtgga gatcaaaccg gggaaacgaa ccgaacgtgt atctacaccg 240 aaacgttgtg gtagtagtca ctcaaaagct cgccactgac cttcgttact ccgtcatggt 300 cttgggacgc tgaatagtat cctggggggt cttatcctta ggatatcatt gccgaaagca 360 ccgatagage tgggcgtaaa cactgcacaa ttttttcacg agctacttcc agtgtattga 420 aaagteetee cagaccaata teeatgetaa etgaggtttg gettetgeta eggeaetgag 480 aagggcagcc aattgtaaat cgtatctact ttatacttat ccaccacttc tgctatttgt 540 tggcattggt gatgtctact atttcggcag gacccgcttt cgagtagtcg cccttaggct 600 ctgcaccggg gatataaccc gcttcaacgt ttccctggga taacgctttc tcaactccat 660 agtcaactcc gatccgatc 679

- (2) INFORMATION FOR SEQ ID NO:144
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 611 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...611
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

60

120

						1
agaatgcgat	cgttcaaaat	atatgcagat	ggacgacaac	aagattgctt	gtgaagtctt	180
cgggactcct	aacggataga	tggtcggaca	agggtttgtg	tttctgacgc	atctgtcttt	240
		gaaatatacg				, 300
cccttgggac	aaacttcttt	atgcgaaatt	tggtgggatt	atgtcaggag	taaagagtct	360
tttataacct	ctttcatttc	tccgacagtt	gtcaaggagt	ggatgtctat	actttggccc	420
gggaagataa	ggatcgaaag	taaactccgg	tgtctgaggt	gttgcttttc	gacctggctg	480
gcaggatggt	cttcggcaaa	ccattgataa	taaaatctat	tcggacatag	atactaacga	540
		acgtagtctc				600
taaqqtqcaq						611

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...648
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145

60 cgatggtttg ttattcatag aagagttgcc taagatctta caatatccgt agtggtgttc tttttcctca tggtaatcaa tagtataaat ctaattgagg aatcgatgga ttggctacaa 120 180 gtotggtgot totggggatg ttatttttat accattottt atotatgtca atatgtattt 240 atatgtaata atctgttgtc tgttattggt tgcttgggag cttttcttcg gatgaatctt 300 tatggacaac tgagaagcga acaaagattt tcatgggaga tacgggatct ttaatttagg 360 cettettttg agetttatgg cettaegett gettaecece atteaaatae tgetttaeet 420 cttccatatg tagtagetee getaettatt cetggttega tttattccat gtttttgtat tgagaatttt atcaaagaaa atccttttaa acctgataag agtcatattc atcatagact 480 tatggetttg ggttgaegea gagacaaaca etgttgteat attactatae tetategegt 540 ctctttgtta atatctttgg gtacccattt tttaatatca atgtgctgtc tgctggatat 600 cgtcatatgg atcacatcca atatgcttat agccaatttt cgcgcaaa 648

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 673 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...673
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146

cagtggtgat	ccgagatatt	catagaaaag	cagtgcgacg	atacgaagac	tgcgagtgga	60
		attctctgac				120
		attaaggcag				180
		gttgaatatc				240
		tgtgtaaagc				300
		cgatgaatac				360
		aatccgatgc				420
		gcagttgtgg				480
		tacgatctgc				540
ggatatccgt	tttcaagttc	tgcgcattga	agagetgete	ccttctccca	ctacacgata	600
cqqacqcttc	gtgctctctc	catgctgtat	cctcatctcg	gttcgccctc	ctgatcgggg	660
cggacaactg		_				673

(2) INFORMATION FOR SEQ ID NO:147

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 556 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...556
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147

cggagatttc	atacgagcaa	ggcaaagaat	cgtatgcccg	cagcaaagac	ttttcgacaa	60
atcggtcatc	getetegaag	agttcgaggc	agccgaggaa	atttcgccaa	aatcaaagag	120
gaactgtcca	atgcgcgtga	agccatgaga	tcgtaaagaa	aggtgccagc	agccgtacag	180
		tgcgcagcac				240
		tcaggccaat				300
		atttttgtcg				360
		gcatttcggt				420
		cagggaagta				480
		agcgacagag				540
agategtact						556

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 713 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...713
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148

ccaaaaqqqt acactctcqq aqcaatacac qatqactcqc cqcttqcaqa aqcaqccqqc 60 accoctctcc tcatagcact ggacggtgag tggggtttca catgcgtctg aaagatgccc 120 cacgetteee tegeaatatg ggettggaca ccaaaaagac aatcagetee tetacaacta 180 tggtcgggag gtagcggcca atgccggctg atggggattc atatcaattt tgctccggtg 240 ctggagtgaa caacaatccg aagaaccctg ttatcggcac gcgcagcttc ggcgcaaccc 300 acqccqaqta qcaqaaaqaq qqattqccta tqcacaaqqa ttqaggacgg aggagtgatg 360 gccgtggcca agcatttccc cggacacggc aaaccacaga ggactcgcac aagaccttgc 420 ccacggtctt tgcctcccga gggaattgga gaatactgaa ttgttcccct tcaaggagtt 480 tttccgagcc gcctcagcgg agtgatgacc gctcacctca atgttccggc tttggaagca 540 600 agaaaaatac gccctcctnc ctcagtcatg ccatctgcac cgatctgctc ggcaggaaat gggtttcaag gggctgatct ttacggacgg actggcctgc caggagtaca gaccagccgt 660 tettaaaceg atetteegee gtgeeaattg geegeaatga cateettete ggt 713

- (2) INFORMATION FOR SEQ ID NO:149
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...465
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149

gacgatgatg	atgaatatgg	agcgtcggag	cggaaaaatg	aagcccgtgt	tcgaaaagca	60
ttggtggata	tggatggtga	accgtaccga	gcattgcgga	gatgcgtcgc	gaatgggcgt	120
tgagcaccga	gtacgtttac	cccggccgat	acagttcttc	ggccccgaac	atgtatgcga	180
tagccccacg	atgacatccg	cttggaaaag	aacgatcgct	gactcttccg	ctgcattagt	240
cgggtgataa	gcagttgctt	ctgtttgttt	tgtcgaaaaa	aaatgttttt	ctttcaataa	300
gtctcattta	aaagaatcgc	ctatcgacgc	atatctacct	tctaacaata	aataaagagg	360
attctcctat	gagcagtttc	cacaagctga	ctatgatgaa	ttggtcagcc	tttatacaga	420

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 670 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...670
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150

cgctggaaac ctgaaggagg tgtgcccgag gtactggaga ttccggccgg gagcaagaca 60 aagcgaaaga aatgcatcag gctttggtgg aggctgcgcc gaaaacgatg agagcctgat 120 ggaaaaatte ttegateagg gaagtettet gaagaggaga tgegegatgg tateegtgee 180 ggtctgatct cgcaggtatg taccccgtgt tctgtgtcag tgcggagaag gatatgtgtg 240 tgcgcgtaca ctggagttcc tcggcaacgt ggttcccggc gtgaacaaac tgccgcacct 300 gtggctgtga gcggagagga agtgaaaccc gatgcttcgg ctccctttgc atccatttct 360 tcaagactac gatagaaccg catattggtg aatatcatat ttcaaagtaa tgagcggtac 420 cctcaccgag ggagtagatc tctcaatgct gaccgaggct ccaaggagcg catcagtcag 480 atattegtge ggeeggacag caacgeatea aggtggacea gatgtgtgee eggegatatg 540 gagetactgt gaageteaaa gaggtacgee gtggcaatac getgaacgaa aaggegtgga 600 gcatcgtttc gacttggtca aattcccgag cccaagtccg tcgtgccatc agggctgcca 660 acgaatccga 670

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 963 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...963
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

```
accgacagga taggtttctc cggataggct tccatagcct cgataacgca tcggaagaaa
                                                                        60
gggctgtcac gcggaaaggt ttcggcactc tgcttgacgc ctgatgatgc aggctattga
                                                                     . 120
cacccagcag ctcgccatcg cttaggcaag tattcgtgcc aagacggaat cgccctgtaa
                                                                       180
acggacttgg tgtgcccaaa cgatatgggg attttcggat taagccctac cggattttcc
                                                                       240
gactggcata tatatectga tacattecte egeegaaage tgtegcaagg agttatgeee
                                                                       300
ccggcaaata ccgaggatcg gcacattgcg gcgagtggct tctccaccaa tagcagttcg
                                                                       360
ccccgatctc gctcgggatt gacttcgccc aggtgggaat ggggtcttct cccaaatagg
                                                                       420
acgggagtaa atcgtcccca cggaaagaat cagcccatcg atgaacgtgg cataatgacg
                                                                       480
tatgacctct tatccgtagt caaagggata agtaagggta aacctcccgc acgtattacg
                                                                       540
actoggtata ggctctggca atacacgagc ccgaggtatt ataattcgtg tcaaaccaat
                                                                       600
aacaggtcga gagggagact ctcctccctc aaaagctgcg gcgcaccgtc aagctcttca
                                                                       660
tagagetgte ggagegeege aggatatact gatagttett aggactaage atetattett
                                                                       720
gcataagtag catttettet ataaacteee tgegeggace tacetegtet eecatgagea
                                                                       780
tggaaatatg gcatctgcct cagcagcatt ctcgatcgtc accttacgaa gcgccttttc
                                                                       840
teeggateea tegtegtett eeaaagetge teetegttea tetaceaagg eeettgtaeg
                                                                       900
cttgtacatg cacacgggtt tcattaccat cgcataacgg tcgacaaacg cttgacgctt
                                                                       960
gtt
                                                                       963
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...682
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152

acgttgccct	gcgatacctc	catcctgctc	aaacgagctc	ctcacacgcg	cgaatgatcc	60
gtctgcgtcc	gcactccttc	gccgaaaccc	tgaggcgtag	ctcatgtggg	gagcagccgt	120
aagataaaga	cacttgcgac	ggtggacacg	agccaacgga	cacttaccat	agactactcc	180
			cgcaccgaag			240
aaccgacggt	cgtgaatcac	gtatcgatag	aggttcggca	aggagagatc	gttggattgt	300
			ctttctatat			360
caacgaagga	cggatattcc	tcaatgatca	ggcatcaccc	aataccccgt	ctacaaacga	420
agcgcgtgcc	ggcatcggct	actggcacaa	gaggcatcca	tattccgcaa	aatgtccgtg	480
gaggacaaca	cctctccgtc	ctcgaaatgg	ccggactgcc	caagacctat	cagcacgaaa	540
			tgagaaagta			600
			tagcccgtgc			660
	acgaaccctt					682

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 973 base pairs
 - (B) TYPE: nucleic acid

102

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...973
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153

aacgatacgc ttaagctccc accggagaag attgtccgtg gtgcagtgcg atcgtccaga 60 tgcagacggg taagaatctc ccgcgcgcgc tgttcgtatc ccacgcgcca agggcatcca 120 tttcggggag caactectee catgegttge egtegeeceg ageegaagee teeteecatt 180 gcgctatcag ggaggtatct catcgttgtg tccgaagcag gtctccagta cggtactgcc 240 cggaatactt ggggaagctg tggcaggtat gcacggcgga taccgttttg gtagtcactt 300 ctccggaatc gggtgagtcg attcccgtaa ggatattcat caggtcgttt tcccgttgcc 360 gttgcgtgcg ataagtccaa cettttcgcc cettcgatae tgaaagagag gtettcgaag 420 agaaccaaat cgccgaaact ttggtcaagt gctgtgcctg aaacatgctg tctttagatg 480 cagtagtggt tcaatcette tgtttgtatg cetgataacg agecattacg etgegtacaa 540 gttgategte teegeacete geagatagee ggagegacag acaggatett atagtagtta 600 gggtetttet tgaggeggat gtatgeetee aegttatgte ceataegttg gggttgeece 660 cgtacttcgc agccaaacgc cttgcgccgc cacgtgaccc gagccggcat tgtaggcagc 720 gagegtaaac ttgagtttte tteeggatee gttaeategg gaaattegtt ettgaaegee 780 aacagcateg gatggagace gegtacegaa aetteeggat eeagaagtte etgttgtegg 840 ctccgaagcg tcggcctgtc ctcggcatga tacccatcaa actctggcac cggaccagcc 900 tacgataccg gcattgagcg cgaatccgtg gaggcgatgg atgcagcaga tgccaagacc 960 agccgagccg aac 973

- (2) INFORMATION FOR SEQ ID NO:154
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...343
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154

atcaggatcg	gcagaaagaa	tgccggctgc	cgaagtcggg	tgtcatagcc	gactggctgg		180
					ctctgaacaa		240
tagcaggcca	acagcaccga	ataccggatg	ctacagcgcg	ccctcgccct	tttcgcggag	76	300
agaaagagcg	tctgacaccg	tatttccgcc	agatgaatct	gac			343

- (2) INFORMATION FOR SEQ ID NO:155
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 664 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vì) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...664
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155

cccccgaatc agagcagtat cggatcgacg ttgtaccaga taaagccgtc aaggtgtatc 60 ggacgaagaa agcggtagtg gacggtgtcc gttacagcgt cagcggaatg tcctgtgcaa 120 tgatgtegea tgeacceegt egeaacette aaggetetet tteeaattet ttteeagace 180 gatttctatc cgaatgcact gatttccgat aaacgacgtg ctacatcgta aacaaaaccg 240 geggtgaate etgteecaca taatagtete tgteattgta tegggeaatg ateceageae 300 ttetttettg gggnaatttt cagggataat caegeaaega ateaeagegt eeceaeegge 360 agececteet ceaceacagt ggegeaaage aacateaega taaggacaga gateagtaaa 420 acgccgtaga gagcaatctg ttcttcattt ccatttattt attgaagtcg atggcaatac 480 ccatacgcag ccacgagggt tgtacggcgt atgcaccaaa gagaaacgct tgctatccag 540 asagcotcag ccagattgtc atttcaaaga agaaacgtga gcgcttgagt ggatattcac 600 ataagcattc atcagaggga aagaccctcc acctttactc ttgttgcgtg gtgaatgctg 660 664

- (2) INFORMATION FOR SEQ ID NO:156
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 656 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

60 ccgaaccaat ggcttggcta tatgccggag gcgatcgtag aatcaacaag tggtggggga 120 ataccggcaa tgctgagaat aagccgatca acttcttcgc ctgacaactc gcggtggact 180 tqtatatqac qtqccqatta ttacqcaqaa qqtqctattc cqqqaqqqca qtacttacct 240 tttgccaaag gcttatggcg gataagccga gttatacggt ttataggaat cgtcattaca 300 tatatgtatc aagacgctgc cggataagat agaagtgaag tattctattt gcgatggaat 360 tttagtaccc aacgatactt atatgggcta tggctacaac gtggagtcga tgagcaaggc 420 aatgtcacca ttactaatac gatgcagaat tggatcccca tgttgtgaga ctcgttgcta 480 aaaatggtgc ttactttggc tccagcctac cgatacttcg gttgagtttg ctgagttagc caacggtgct cgcaaacatt caaagtaaat aaagatgctg tggcggtcgg ttctgcttac 540 600 tggaggttta ttacaacccg gatccgaatg caacagggtc gttccggaaa agttttatca 656 agaaatagac agacttatga aaaagtattg gtatatgctc gttgctaacg agtgtt

(2) INFORMATION FOR SEQ ID NO:157

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1128
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157

aaggtttcaa tttcgcacaa tgagagatcg tttttttgtg caaaggtgtg tttctccttc 60 120 togagatatg toatotttaa ttocattatt togtottaga accgaacaaa ggtagaattt 180 ttaaggagaa ggataaatga aaaaacctta aaaacatgaa agtaggagat aagtgtgaga 240 atgagtgege etgatettgt gateggegea etettttegt tgtttggtee tatggacagt 300 ctattgtatc cggatcgtat tcgggttaga gccctcctcc tcctgatccc tgatgccacc accggtttga gaattgctat cgcctgcatt ggcagaagca cctccggaag cggcttgccg 360 420 tactoggega acttoagato oggagogato aggtacaato cogttogoga gtgacogtat 480 tgtaacgaca ctctgccctg aattgacccg aacggagttg aactgggagg ctttcacatc 540 ctetttette ceaeteeega teetttggee tgtgcaatga gaeggaaaca accgatgeet cgagettgat ettettgeee gaageeaatt eeetgegeat gaegatgeea aategegeag 600 gataccgaat acategeeeg ggetggetee egaaagtetg agatttgtte tgegatgtge 660 720 agggtggagg caatgctgcc gttgatactg tctgcggata ccacagcttc ttgcctgttg 780 ccttgtgggc aatacggatt gtcttctttt gaagaataac ataataattg aaagaattaa 840 tgattaataa tgcggacttt ttctgtccat taatttaata atagcaatcg agaatcgatt 900 eggegecate etettetete tgtttgeact geaaagataa ggtaaagaaa etgategtee 960 aaatgttttg cagaaaaaag ttttcaacaa caagggcgct ttacgcttta tatataaaac 1020 ggcttccgta tttcttatac aaggettcga agcactette eggetttegt aaggggaget gaaatccggt attcggcgtt gtccgaatga tttatatata aagtattttc gattaataat 1080 1128 aaatcgattt ttatttatat attaatcgtt ttcattttgg gggatccc

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1021 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1021
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

cttgtattgt gcatgttcaa ttgtttgctt ccgacaggtt gtcggcttag cttcgggagt 60 120 agatacagtt tcattcagag tgattgccgt aggagtgacc tgatcaaacg gcgacgatag 180 agcattccga cagccatttt gaacgtttct tgctcatacc ggtatgttgc ataatttcct 240 cgggcgaact cttatcccga tgggaagccg accgcctctt ctttggagca tgtgtagcag 300 tegttgetet eggagteaat aeggteatag eetateggtt tgagegagag gtegttttae 360 catcytcacy gaggcgaatc acgaaagctt tcacttytyc cccatagcca aaggcatcyg tagogtatog gaatagatoa tococcaatg ggatgatoca cgatcatgog ataaccogga 420 480 togattogtt ogtaaaccag toogacacct tgtooccagg ggagtaggat gggggaatgt 540 tgcccaaatg ttggacaatt tcgccgagcc aacgatctta ccgctcacat gatcgatata gcatagacga aatagcgtcc gccttctcga atgagctgcg tctgttctga aaaggaacga 600 660 agagateett gtgtatgeee catteeatat aegeeeeta tetgtgaegg agaeggeatg 720 cagcagagee acctgteeca ettegaaage ggeegeatgg tggtggegat gagtetgeet tcattgtcat gatagcgaat acctccactt ccataccagg tgcagcatct gaggggaggt 780 840 agogttgggc aacaaaatat cogtatogoc tocatogaga tatgococaa tggtacgata 900 eggtegatgg teagaegaee tatgegteeg agetggtatt tgteegette atceteeggg attactcaag cgtaactgac gattcgtcgc gaggacgggt tgcaccaaaa tagattcggg 960 1020 cataccatcg cgctgcacct aaagacgcac gaagtaatct gctggtcgtt tacgtacgaa 1021

- (2) INFORMATION FOR SEQ ID NO:159
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 735 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159

gateteett	tttcatcgtt	agctgtttcg	tttttggtat	agggtgaata	caaagaggct	60
gtgctcttgc	: aggatcttgg	aacctgaaag	cacagcctgt	ctattgctgt	attacatgag	120
accgcgagcg	, cggagcaaat	ccctgattca	ggcttttgca	gaccggtgaa	cgcggtgaag	180
	aatccttgta					240
	: ataccaccgt					300
	aagcgtagta					360
aggagcgata	gcgaggaggt	atctgcggat	tgagagaccg	actttgcgca	gggcttcttc	420
ttcgaacttg	gccacgtcgg	tatggcctcc	gnctcttcga	ccgtgagcgt	atgccatgcc	480
tgatcgaggc	tacggctgca	agattttctc	ccatagaata	agcctgattg	aagtcgctcc	540
atcctgaatc	ttcttgacca	attcggccgg	cataggctcc	tgtgtcttca	gtgcttagcg	600
tagttggcaa	acacttccgg	atccatagcc	caatgttgnt	gagetgagae	ggcatctcga	660
cgaagtcacg	cgccacattc	gtaccgagag	caaaggatac	tgctgggcgg	gaaacatacc	720
gtggagggca					-	735

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1093 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1093
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160

egggeetttg	ctgtttctt	cgctgagtac	ggcacatgcc	gatatgccgt	ttggtcttcc	60
gtcatccata	ttctttgggg	tgtcttgcct	ctggtggtgt	tcctctattg	gctgcttgga	120
tcattcgttt	cacgagecet	cggacactgc	ceggettetg	cgcattcccc	aaatggcttt	180
ttggctatgg	gttacccgct	ggctatcatc	atggccaaaa	cgacaggcta	tgtgatggca	240
caaggtccga	cagcatccgt	ttggagetge	tgttggcgtt	gggtggtctg	cttacttgtt	300
gccttgcaat	tcgggttggg	cangtggcta	agcaaacgat	attgaaagag	agcattacgg	360
ccggtcaggc	tttgggacag	aaaaacacgt	cgttgccatt	tggatgtcgc	ttacctattt	420
gaatccgata	gcttctatcg	ccctgcaagc	tatgtggtat	ggcaaaattc	gctcaattcc	480
atccaaatct	gctatacgat	aaacgaaaga	ataaaaccga	cagacaatga	aactaacagc	540
cgatggttac	ttccatcagt	gaggatgaga	agggcaacat	agtattcgca	atggacgctt	600
ggagcttgac	gaattccgac	tgagtggcaa	gctgaaatcc	gaatcgaaat	acgctggccc	660
tacgaagccg	acgaacaagg	tctgccacag	aatcggcagg	caaacggatc	gaagagatcg	720
agctgctcat	ccgtaggcta	tggaaaagga	caagttggcc	atcatgacag	gcaactatac	780
cggagcggaa	caaagtattg	ggtctattat	gcccgtactg	aacgagtatt	cgggaacggc	840
tcaatgaggt	gttggcccct	tacgaaacat	taccgctgga	gaagaatgcg	aagtcgatac	900
cgactgggaa	gagtacctcg	atatgctctc	ctgaaagacg	aaaattcgat	atagccatta	960
tgccatctct	ctgtggcgag	ggagctattt	tttattggtc	aagcttcnga	accggatcga	1020
cgataggatg	attgcgcgga	tggtaggtct	cgatttcatg	ccggagtgtt	tctctqtcat	1080
atgggtatag			-	22 3 3	3	1093

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 721 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...721
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161

taceaatcan ctc	tagagga teceegace	acagcatttq	cgtcacggta	ggggcgactc	60
agtaggeegn eee	gegeega teagaacga	datacaddca	cgacgttgat	ggtcatctga	120
egracecaca aac	erecest staggadga	gadateatee	ccacataacq	getttggeaa	180
aagaggataa aac	ggcggat attccgaaa	gegategeee	+-+++-	agga at acc	240
tgctgctgaa aga	atttcca gaatggtga	t gtegetegee	tetttggeta	eggeagegee	
ategeeateg aga	ggcccac ctgtgcgcg	g ttgagtgcag	gagcgtcgtt	cgtgcgtcgc	300
ccatcacaaa cac	cactttg gagagette	tqcaqcaqqc	gtaaagcctt	tccttgtcca	360
terrorrange and	ggacatg atacgcagt	cactatecaa	gggcgcagtt	cctcgtcggt	420
teggaegage geg	iggacaty acategorage		tagagettte	atcccacage	480
tagggctgcg aaa	tccgacc cgtgatcat	tteegeteeg	Lacagettee	geeeeaaaa	540
cctatttggc acc	gatetee egggeggta	c ccggtgtatc	gcccgttacg	attttcaccg	
aatgccggc ttc	atacagt cgctgatcg	ttcqqqaacg	toggagogat	ggatcggcta	600
transactat aga	catgaag cggaggtca	gcacqtqaqa	cacccattag	caaatacctg	660
tgeegaetat acc	cacgaag cggaggcca		gasttaatta	cctdatttcd	720
ctcttgtcgg agg	gacagete ttgatgaaa	L eegacggtae	gcarragerra	cccyaccocy	721
q					721

- (2) INFORMATION FOR SEQ ID NO:162
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 637 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...637
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162

aagcactcct	ttctgtagaa	caagccgtgc	gcatgtacac	gaggcgcgtc	cacatcaagc	120
tctaggggcg	aaaacgccta	tgcaagtatt	gcgccagagt	ctaaaaatcc	gttactggca	180
aggatcgaac	attggcggag	attgcccccg	agctataccg	aaggatgaat	gtcagacaaa	, 240
gagctacttt	gctcgtgtca	accgaaatta	gacttaaggg	taaggggtgt	caactaaagt	300
agaattatag	aaagaaccag	taaaccaatt	gtagaactat	cccccaact	gtcaactttt	360
ttcagtacac	gtcaagaaga	gaatactaca	gacatcatac	tgctatcggt	atcgatcgtt	420
cagggatttg	ctgccggagt	gaaagactgt	cggtgccaag	cgcatcgatg	aataaggaga	480
tccctgtact	gtagtgcttc	cggatatagc	cttggcgagc	gagggcggag	attgccccgg	540
gtgtacctgc	tgcatggcta	tggcggaaat	gccgaacatg	gctaaccgta	aaccggacct	600
ccgcagatag	cagatcaaaa	agggatcatc	ttcggtt			637

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...652
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

```
gctcaacaag agaagcaggt gtttcatttt ctgaaccttc cggctactga caggctttgg
                                                                        60
ctgccggagg caaagctatc accatcgtag acgacaatcc ggactggctt ttgagaatcc
                                                                       120
ggctctgctc ggatatgaat ccggtggcgc gcctttcttt cctatttata ttatatgagt
                                                                       180
ggttcgcata tgggcatgcc tgttatgcct cgtccgtcgg agagcgtggc atgtggggtg
                                                                       240
ttggctgcgt ttcctgaact acgggtctat gcaaggatac gatcagaatg cgatgccacc
                                                                       300
ggctctttta gtgcttcgga tatagctgta caaggatttt acaccatgaa ctgagcaacc
                                                                       360
acttccgcgg tggagtcagc ctaaaagcat tgattcttct atcgagacgt atagttcctt
                                                                       420
tggccttggt gtggatgtcg gatcagttat tacgacgatg acaaaggata ttccgtttcc
                                                                       480
getetgttea gaaegtaggg gegeaaetga aaggetataa tgaagaaegg gaaeegetea
                                                                       540
ttgggattte cagetegget tttecegeag ttttateaat geteegtteg ettgeacate
                                                                       600
acgttgttca atctgaatcc gcactatttc aagcgtctgt accacgcgat ct
                                                                       652
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 715 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...715
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164

tocccaattc	tcatcggttc	gtttgaatcc	gcgaatcctg	ctcagcatac	ggaagcctgc	60
tecetatega	ggaagaggca	aatgaaaaag	gcaaggccct	aacggtcagg	cattctttc	120
agtaggetec	acttatcaat	tgttcctcct	attetttace	aggacaaagt	cgtcgggctt	180
gazzastat	gceaacacaa	ttgtgctctc	ccacatacca	aggagtatgt	cccggtaata	240
gaagaaacec	gtaaacgcga	acttcgagat	actogaatat	agtgccatca	agccattgtg	300
aaggactgat	gccagggccg	acticegagae	agastaaaga	tetteateae	cetttaggee	360
cgagaagtca	ttgcgcagga	aatcaagtaa	ayaacaaagc	tatasata	tacaastaas	420
gaatcgggat	ccacaccggt	cttgctatca	tgtetttte	gatetyaeta	cccggaccga	
aataatggag	gaaaggcaga	tgcgtctgct	atggccatag	actttggtcc	agcgatcgac	480
ggagaggagg	gatcacaaag	aagagattgc	ttgagcgact	cttcattcaa	tttcttcttc	540
ggagagttaat	acasacatas	ctttcgactt	ctatcaaatt	ctctcqtqqa	ggttgagata	600
cyaacccaac	testaggest	cgtcttccac	tatacaaatt	gacctttatt	ttcagaagca	660
aagteegaag	tactgeggat	cycoccocac	thetetaca	antetataaa	atata	715
ggaactgtat	tcataggttt	gagtttcttg	ttetateage	yacacacaaa	acycc	, 13

- (2) INFORMATION FOR SEQ ID NO:165
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...724
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165

					++~~~	60
caaccattac	agaaggagat	gcaaatgcgc	agcgcaacct	egatatgete	ccggcaaaaa	
ataaataaaa	ttttccatat	tgattattaa	ggtgcaccgg	acttctgttt	cggtgctctt	120
gcaageggag	t to the total		+-++++	taccasaart	tttcaacgac	180
ttttgtggca	aatcaagtcc	gcatgcacaa	tgtttttatg	cyccaaaayc	ccccaagas	240
gaggaggaat	ttggaacatt	ccaqataatc	ccctttatga	aaaccgaatt	caaggagaaa	240
atgatgtata	atgattttc	ggataggaag	gcctttttcg	tcaggtcgaa	caacattcca	300
ucgucgogog			+	aaccettted	agtgettett	360
cccaacctga	accatagacc	cagaaaaaac	taaactttag	aacccccccg	490900000	420
gctaaattta	tcttagtgtt	gcatttqttt	gtggatgtgt	acctcaaatc	gtttaggaga	420
ctattgaaga	aaaaaaatta	tttcgcgagg	taaaatgtag	gaatacaata	agattcacac	480
Ctattgaaga	uuuuggueeu			startatasa	actocaaaga	540
atcaagatag	atggcacaac	aggaagatet	cttcaaaaaa	acaycoccac	accycaaaya	-
tacqqcttcq	tettteette	atccaagata	tacgacggtc	tggcagcttg	tacgactatg	600
	L-L		assacacect	aataaaaaa	tatgaccctg	660
caccaaatcg	tctgaactga	agaacaatat	caaacgcact	ggcgggaaag	caegaeeeeg	720
cttgcatgat	aatgtggtgg	gcatcgctct	gcatcttcat	gcatcctcga	tctggaagct	720
		, ,				724
tcgg						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1079 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1079
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166

aacaaggatg ctccatctgt catttttcca ttcgttctga ccgaataggt gtagttgttg 60 atattctgat ccaattcggg atagagggga atggtattcc attggcatcc tcgccggtct 120 gccatgaaag gatgggcatc acgtcatgag ttcatcacgc gtatattcgg ctccgaacaa 180 aagttgcgaa ggcatgggag gaatttgtcc aagtcgtagc tgtactggat accgcccata 240 tatgtttgcc tttggtcacg ccataattat tgccgtattg atcttgaggg ataggtagcc 300 ttccgtacca ccggggtggc cattgacgtc aatctctccg atactccgta atagctcttg 360 420 gategtattt caagttteeg caaataeget atggteagtt tgtteageta caeceactae 480 gtgaggaggc aatcgatacg atcgccacca cggcggaatt cactgatcgt gtgaaactcc 540 ccgtcaattt gctgtagtcg ctcaagcgca aataagaatg cgctcccacg agcgggcatc 600 tattttaccc aatteggaat aacegteatt gttageacce aatggttgeg gtaacgagee 660 tgcccgaata ccatggcacc ggcacgttgt catcgctgac gatggaggca ttgaagttcg 720 tgttgttatc cagctgctga aaccggtaaa gctcagagat tcattgaatg tgaaagaatt 780 gtgaaaggtt cettggtgat gatatteace acteeggeaa tageagaaga acetacaagg 840 eegateetee accaegtaet acetecacae gttegateat atggeaggga tetgeteeag 900 accytaaaca ccyycaagyy cactcatyat ygacyyctyt cyatyagyat ctytycataa 960 cgaccatcca gtccattgat caacttgatt gaaaccacag ttctgacagt gttctctaca 1020 cgaactcccg ctggatgaca agccttgagc cagttagaag catgacttgc gagaagact 1079

- (2) INFORMATION FOR SEQ ID NO:167
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167

cgggcttcca t	attggaagg	atattcgtac	ggtaagcgta	aacaaagaac	ggcgcgttcg	60
tcctttatga c	ctatgccga	ccgaagcgaa	gctctcacgg	caagtatgag	aagagttcgt	120
actaccgtct to						180
tgccggcata a	cggatgctc	ggcaaataca	aagggatggc	ncgacatcca	agtncccggc	240
aactggagat c	aagggcacg	gngtggccat	ctataccaat	cacggatacg		290

(2) INFORMATION FOR SEQ ID NO:168

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 664 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...664
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

tgtattggaa ggtaacgaac ctatcgttat tacaaacagt gagggcaagg cacaacgccc 60 tcggtagtgg cttttgtgga tggtggcgag cgtaaggtgg cgatccggcc aagcgtcagg 120 ccatcaccaa tccgaccaag acgatatete tatcaaacge ttcatgggeg aaacttacga 180 tcaggtttcc agagaatgga gagagtgcca ttcaaggtag tacgtgggga caataatact 240 ccgcggtaga tatagacggt cgtctctata cgccgcagga aatttcggcc atgaccttca 300 gaagatgaag aagacggccg aagactacct cggtcaggaa gtacggaggc cgtgatcact 360 gtgcccgcat acttcaacga cgctcaacgt cagcaacgaa agaagcagga gagatcgccg 420 geetgaaagt tegeegtatt ggaacgagee taeggeaget tetetggeet aeggtetgga 480 caagtccaat aggatatgaa gatcgctgtc ttcgacttgg gtggcggtac cttcgatatt 540 ctatcttgga attgggcgac ggcgttttcg aagtgaaatc gaccaacgtg atacgcacct 600 cggaggagac gacttcgacc acgtgatcat tgctggcggc agaagagtca agtctcaaga 660 aggt 664

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...450
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169

cgcgcgttgc catctactat	ttcaaaggac	cgggacaaaa	cagcctcgtg	cacaaggaat	60
agagaccetg cettetattt	ataatgtatt	gcgcaagagc	agagcgaagg	ctatgatctc	120
accggattac ccaccgatga	agcagetteg	aaaagatcat	catgacgcaa	ggagctattt	180
tcaatagcta tgccgaggca	atctggcacg	ctttaccgaa	agcggctatc	ctgcattcgt	240
acccaaagtg atttgaagca	gtggatgcaa	gaagtcctta	cacccaatca	aattaacatt	300
tgcaagaacg ctatggagaa	geteeeggag	aatactattc	gatgagcaaa	acggagtagg	360
cggcatcggt gtaacccgtg	tgcaagttcg	gcatgtcgtt	cttttgcctc	agcccgtaca	420
aggtggaagg ggccaacgac					450
aggeggaagg ggeenerge	- 33 3				

(2) INFORMATION FOR SEQ ID NO:170

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...501
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170

ttatgcctca aaaattttat attcaaaagt ttttctccca tttcaataag cttttgacat	60
tttcttctgt tgcaggctgt attttatgca ctccaaattt ttagcgatat caggagatag	L20
ttttagcaat totottootg totgattatt coaatgatta caagottggg atatttggga	180
ttggcaacat tgtctgtgca agctttgcaa tattagacaa acgcaaactt caaatgggtc	240
aacaatctat ggaaatcatc tataacaaaa tttcctccct cttcaaaatt actataatga	300
gttgatttat thtcgtcgtt tcatctatat ttcttgctga caatattcaa aatgtatttc	360
ttettttatg teagataata tetteaaaat agagaagtet teeetgttee agtttgteee	420
totatgataa etggettett ttaettgtta eateaattag aattttegta gtagtttagn	480
ggttcgacat tgttaagtgc g	501

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 566 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...566
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

cggcttccat gtccgtatat ataatagcac gcggagcaga aaccgcttgc acttcatgcc 60 cgttatactc ttgaagcccg tatagtagtc ccagcagcat ggccgtatat ccgagagcta 120 ttggccatat gcaggggata gccttgagtc ggcctgcgag tacaaaatcg tttctgtcaa 180 aagccaaagc cagcacagaa aagactcagg catactttgc aggcattcgg gatacgaacc 240 300 cccgtttgcg aatgtccata ttgagcggtg aagcgttggt caaattgctc acctctccaa aaattotoca ttoacoggaa tgaatacoto ottgooggoo atacoggacg aacaaacaga 360 420 taaagcatgg aatcacgaac cgaaacttcg ccaagggcaa gagttcagga aaaggagagc 480 gttccgtacc gtaaatacct ttccatacat atcgagaaat tcgcccatgg ttcgcagcac ttcggattca aaggcaatat ggagccattg ccttcatgac cgatgttcag cagataattc 540 566 ccccacgaca caccactcgc accaaa

- (2) INFORMATION FOR SEQ ID NO:172
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...386
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

60
120
240
386

- (2) INFORMATION FOR SEQ ID NO:173
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 915 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...915
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

60 gggtagcgga ggtctctact tggatcatta tcagggagat ccgaccgtca gcctgttgcc 120 atoggaggtt atgotocatt ggagcaagtg tatgottaaa tootttgoog aaagaattgo 180 cggccgataa gcatcgctac gtgctcgagc acaggccaat ctgtgggcag aatacctcta 240 tactteegaa egataeaeta teaggeetat eeaaggetae tggetgtgge agagettaee tggacccgtt ggccaagaaa gattttgccg atttctgtcg ccgtttggat aatgctgcgt 300 360 tegtetggae atgeatggta teaattacea catteegetg eecaacaace gggtggetet 420 tecgaettta tageetttae ggaeaagget aactgaeett eaegaeateg egteegatga 480 aaatggtota tacgotggac gaaccgaacc gaccotcaca togactoott acacggtoco 540 tettgaattt cacaaaeggg eettetgaag attegtaeeg teaeggeegg tgggaagata gtcccqtacq ccqcattcqt qtqqaqaaac aacccttcaa tatgtcaagg aagtaccggc 600 accgaaaccc ggactgacca ttcgtacggc ttacggtact tatatgatgt gcctgatctg 660 cagcaggtag cctcatggga agtaggaccg ttagctcttt ggaggaaatc atgcacggga 720 780 aagagaagat aactttcctg aagtactgga gcgcagagtt gtagaggcta ccggttatgt 840 gcttttccgg aggatggggt atatgagttc tctcggaaaa caaacgaagt tttgattgat 900 aatgggaaag cttgatcgac aatgtgggcg aagttaagaa atctcccgtc tgcaatagca 915 gtcgttcccc ttcag

- (2) INFORMATION FOR SEQ ID NO:174
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...708
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174

agcttgctcc	ctatatcatt	ggtaacatag	aagaagatgg	ctacctgcac	gtgatttgga	60
ggagattctg	gacgatctcg	ctttccgtgc	cggtatcggg	cggacaaaaa	ggaagtagaa	120
gaagtgatag	gattggtaca	aagtctcatc	ccccggtat	ctgtgccaga	gacctcaaag	180

agtgtttgct	gctccattgg	acgattgcc	ggatacgaca	gctcggcaga	cagccctcca	240
tattctacga	accattatga	cgactttgtc	tccaaacggt	tcgagcagtt	gcagaaggaa	300
ccattccttt	tccgattcgg	aaatgaagga	ggccttcgaa	ctgtcatgca	gctcaatccc	360
			gagcagccat			420
tcatcgtcga	gcgcatgggg	gcgatctggt	cgtgtcgctt	actcgtggtc	gtgatattca	480
gcccttgcgc	tcagtccggt	ctatcaggag	atgatgcang	attatcaaag	ctctgctaaa	540
			ttttcgtcaa			600
			gaaacgcaca			660
			agaacttgcg			708

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

gctgtcgatg	agtttcttga	gtttgagctc	gatttgatcg	cagagggcag	caattcggta	60
			aagtccaatc			120
			ttcctcgcta			180
catcgccatc	tgatgcgtgc	cttgctctcg	ctggcgatga	tatccgccac	cggctcggca	240
			cacggcgagt			300
			cgagaatacc			360
gccatggcag	gcaatctcga	ctggatgctc	ggagtgaagg	agtgenggee	atggaaacac	420
			gctccatgaa			480
cgaggcttgg	ttccgctgaa	gtcaatcggc	ttggccacga	tatagaaaaa	gtgggctaag	540
agcggaaagc	attccggacc	ggacacacga	attcaccgga	ataccggc		588

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 815 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...815
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176

60 gegtacegtt etgtaceatg acagtggaga cataacetet teeettgtea gagaagaete 120 gatgatcgaa ccgatggcac ggcggttagg attggcttca gctctaagat atccgcttcg 180 agcagaacct tetecageaa tteggtgtgt tgatgeettt ettggeegag ateteetgae 240 tttgatattt gccacccagt cctcaacgag gtagttcatg tttgcaagct gctctttgat 300 cctttgggat tggcagccgg tttgtctatc ttattgatgg cgaataccat cggccacctg ccgctgaagc atgattgatg gcttcgactg tctgtggcat cactcgtcgt cagcagcaac 360 420 gataatgatg gcaatatccg taatcttcgc acacgggcac gcatagccgt aaaggcttcg 480 tgtcccggcg tatccaaaaa ttaatacggc ggccactggg aagtttcaga ccataggctc cgatgtgctg gtgatacccc ctgcttcccc ttcgatcaca ttcgtattcc taatgcggtc 540 agtagogaag tottacogtg gtotacgtgt cocatgacog taacgatoga ggacgogcaa 600 cgaggtette eteattatee tettengggg caatggntet ancaaateeg egetgacaaa 660 ctccgtcttg aagccaaatt cttcagtacg atattgatcg tttcggcatc nagacgctga 720 780 ttgataccga ccatctaccg atactcatgc aagtggcgat nacttcgttc acggggacgt 815 ccatatattg gacangtcac ttacngtaac naatt

(2) INFORMATION FOR SEQ ID NO:177

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...473
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177

gtacaacggc	tcattcaaaq	ccaattatct	ggtatcgaag	tccggcgaca	atacgtgccc	60
ggagactaca	dcaadaccac	cagtctgaat	atccgatgac	acacagtcag	gatccgaagg	120
ccaatccttt	gcaaacgttg	teggecatgt	caattttqcc	accggnagct	atttccagaa	180
ttcgctgaat	accaccatos	tatcaatacc	catactacta	cgacacgaag	ttcggccgtg	240
agctatcgcg	geatttcca	agtactcctt	tttcgattac	agatagcata	gatacageca	300
gaacatgcgc	caageeeeeg	tanacettac	cttgccgat	cttcgattaa	tatgtccacg	360
gaacatgege	gatacyacyg	anageatata	aaccaaaaaca	ataatacaaa	aagttgagtg	420
cgttatcctt	tcaageggaa	gaccegugua	ggccggagcg	acggcacgag	tac	473
tgggctattc	cggtcagctt	ccaatagtat	cttgacaaan	gagaaagatt	cgc	1,0

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOG circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...516
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178

cgggctgtaa	ctacaatctt	tctcattgtt	ctttacttat	tgtttttaag	ttttgagtca	60
cggtatcacc	ataatagcaa	tcagtgctga	gtttggcacc	gtccttataa	caatcggatt	120
cacttttttg	ttgtgagttt	aatcacaatc	tgtcgagaag	tttatcggca	tgcttcgagt	180
atgcggcgag	ccatagcccg	tcgacatcca	atgcttcgcc	atagctgacc	cctcgttcga	240
tgaatgacgc	tctatttcct	ttatcacatc	cgatcctatg	tgcatttctt	ccagcgggtc	300
ttcagtccga	gttcgcggaa	gaattcctcc	gtccgagcaa	tagtgcatct	atacgctcct	360
cctctgttcc	ctcttttata	tcccagattc	gtcggcatat	tggagcatct	teteeegett	420
gtgatcgtgt	cccaaggtgc	gagagtaccc	ggtagcacta	tggccagcgt	gtgtccgtgt	480
gtgagtccgg	cagtgccgta	tctcatgacc	gatcat			516

- (2) INFORMATION FOR SEQ ID NO:179
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 656 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...656
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179

caacaactee	atcottatoa	aggtaaagga	asttaatsca	ctcacagage	cctgaatgcc	60
cygcaactcc	accellatea	ayytaaacca	gattggtacg	cccacagage	cceguacycc	00
atcgagatgg	cacaccgtca	cggctttacc	agcgttactc	gcaccgctcc	ggagagacag	120
aagacaccac	tatcgcagac	attgctgagc	aaccaactcg	ggacagatca	agacgggatc	180
gctcagtcgt	accgacgtat	ggctaagtac	aaccaactgc	teegeatega	agaggagtta	240
ggccctgcgc	tgtatacggc	tacaagaaag	tgtaagcgac	aaagtacaca	caggtacatc	300
tttctgccga	atacggaaaa	ggggaaaaga	tagtaccact	gccaaaaaaa	gaatgccccc	360
aaagttggaa	acacaacttt	gggggcattt	atttgccgac	ttatttagaa	gcgaacaccg	420
agacccacaa	agaagtcatg	atacgcaaag	aagtcttatc	cggagcatcc	ttcaacatat	480
taagcaatcc	tgctcatatc	caatttgtac	gtaataacgg	togtagetea	aggcagcagc	540
aagcccaagc	ccaagtcgaa	acggttatta	ttcgttatca	ccaaaggete	tacagaagcc	600
gtaacgcctg	caactttagt	cttaatcgtt	ccggcgaacc	atattgccga	aatagg	656

(2) INFORMATION FOR SEQ ID NO:180 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 439 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...439 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180 cgccgactga acgggaattt gcagaaaggg aatgcttgga atattcattg attatcaatg 60 tgattgttac tggttcgatt ttatttataa cgcaagttgt ctcgatattg tctgatagtc 120 tectecagte ecaaatagag ageategeaa teagtgegtg geegatggaa aettegteea 180 aatagggcag tegttegeaa agtaacggag gttgteeaga tteaaategt gteeggeatt 240 gatacgagac cgagcgaatg agcgtgtacc gaagccttga catagggctg tacgcagcag 300 ccatgtcctt atgataggcg gctgcatacg gctcggtgta aaactctatc cggtctgtac 360 ctgtcttggc agcccacgag atattgtcca agcggtattc gatgaaattt ggaagtcctg 420 439 ataccccang gcatggaac (2) INFORMATION FOR SEQ ID NO:181 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 640 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...640 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181 gactgccaag ggtccgctca gtaccgtgat acccataata tagaatcggc tcgagcagag 60

gtggtaggag gtctgcataa tcgtattgag catattggca gacccatgac atgccctaca

tagccgaata tggcgaagaa gagaatgtga agccgagggc ttcgaagaga tgacgcctga

acgtcagttt cttgtgtgag atcttgtctc catttataat gatgtatgcg gtggtttttg

120

180 240

gtgggaaaag acaaggccg		cgttcggtgc	teegeteegg	teetgeegtg	300
aggattatga gttggtgtag	_acgaccctgc	ctcctttgac	ggttgctcca	cgaggttcat	360
accyaaycya caggagagg	i atttgtacga	tggtattgga	qtacqacqaq	atcaccette	, 420
ergeregger egatgetge	gtcgtatcgg	ctcttcctat	agetacaace	ccattastas	480
cadadacede graderier	cgacggtcat	gcccatgtag	agggtggcaa	ggggaagag	540
	gcaactgccc	ggattgaggt	cacteceest	acaacaacaa	600
agccggcgtc gatcatctta	cgggccggag	cgtagtcgca	3	Jean Jyouc	640

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...524
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182

ggagaaagct cgcagctccc gaatcgattt ggtggcagag gtgaagaagc ttacctcagt 60 gtattgttgg ccgaggactc ttatggcgta ttcaagcgag ctatgacaat gctctggcca 120 attataagaa catateegae aagttegteg tggaettgtg geegagtatg ataagatteg 180 agccaatgta caggtagcaa catcgagcct aacctcttgc aagcgcagaa ctccgtagcc 240 cttgcctctg gcagctcaag gtcctgatga gcatggaagt ggaaactccg atcaactctc 300 cggttcattg tccgactata aagaacaagt ctataccggc tatttgccgc cgatacgctt 360 atttccaaca actcctccct gcgtcagctc gaatacagcg tcgtctggct gtcagtgcag 420 acaagetgaa caagtacage teetgeetae acteaatetg ggagggeagt acacetatte 480 gctcaacagc acgacatcaa atctgggcga gggacacgct gacg 524

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183

ggcaaaatcc tgattcgaa	g cgatctaagg	aaaagaaaga	acceteceae	atggcaaaaa	60
gcatccaggc ataggtgcc	t aatagataga	aaggettgge	agggtcagaa	catcctgtat	120
ggtttggage gtatgggta	g agggatactt	ggcgaaatct	ggtacatagg	catccccccg	180
aagagactgt tggtccata	qaqtqttctc	ctgtctgtgc	ctcccaatcg	cgtacgtcct	240
gegeetaceg etggetece	g ctacgtcgcc	ctggaacagt	acacgcccgt	cgaagaggcg	300
ggatagaaat aggccaaag	c gagggctatg	aaaaggagta	cgacgcagca	taaggtagga	360
ttttgcgcca atcaggctt					420
tttcgtttct ttcatgatg					480
cgaccactgc tetetgacg					534

(2) INFORMATION FOR SEQ ID NO:184

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...457
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

atagaaaatt	gctctgccac	tcgtgtggaa	gtctatagcc	agagccaaac	ggtgctttca	60
tatcccagge	atacaatctq	tgcgaagtaa	agaattgctc	gtaacggaca	gcaagataat	120
cacagacatt	gaattaatca	gtggattgtc	ggcataaact	ttgctttctt	ccccggaacc	180
gagtctactt	tetecactee	tatoctctca	atgtggaagt	cgtatcgctt	gacagtggtg	240
atcaaccatt	ctcagagagt	ttatcaatca	ggtatcagcc	aacttcattg	ccaacactgc	300
tacatatcaa	ccaaagtaac	gggaggaaaa	aatcccggtg	ctttgtcggt	atgacggcag	360
atgastccat	gaactgcaaa	tacdacddtt	gctctacaac	aacqaacaaa	necegggtat	420
aagtcaacat	audasacddd	ctcgaaatac	ctgccat	-		457
999009040	~~~~~					

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...472
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185

acgetegeta	tgcagatcaa	ccccatgctc	tgcggttctt	cgttcaagac	aagggcgtac	60
agacactgct	cgatgccgta	tgtaagttcc	tgcccagccg	gcagatactc	ccacagtgga	120
angtacggat	ccttctgact	cgagtaagtg	atagagcgca	agacctctcc	caacgagcct	180
ctctatactt	taacattaaa	attoctacco	accettacqt	agggcgtctt	tgettettee	240
acataattca	agcaaattac	ctaccaattc	atacqtttac	aatgctcgtt	ctgaaagaag	300
gegeatetet	ctcatctctt	ccagatgcac	tctaacaagc	agaccccaaa	naagtgatcg	360
attacaataa	catchatacc	ggtgtagett	cangatatto	gtacqqqcqa	tacgctttgc	420
getgeggega	atactataat	ttcgaatcta	tagacttece	caatccaata	at	472
gatyagagte	accetacege	cccgaaccca	09940000-	- 9 5 5 - 5		

- (2) INFORMATION FOR SEQ ID NO:186
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 604 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...604
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186

		++	ggatatogga	castteaas	acaagcggag	60
gcgcccgata	gtettgetet	egettteeae	ccatatcgga	cyacteggae		
agagcatcgt	gcaagagatt	catgaaatgt	tcggtggtgg	ctgctgctct	tgccccaagg	120
Caccdaaddc	agaccctttg	tagtagacaa	tccttccaga	tcgatcacct	gttcccccat	180
ttaaataaat	tcattcagat	agacatttt	cctgatcccg	tataaccgcc	taagacgatg	240
	atanagatta	agastatogg	ggaaatgccg	acagtatact	ttattccacc	300
aaacgcacyg	graaagerre	agaacaccgg	ggaaacgeeg	9099000900		360
acqqaqacqa	cggatgcgaa	gtcctgctac	ggatagcagc	caacgacact	cregerrege	300
atacctcctc	tccagcagta	gaggatgatg	teetgeegge	agcaagggag	cgagcttctc	420
gcaccatctc	ggccatacgc	qcccaacqaa	ctccaatcct	cgctctacgg	ccgcctggcg	480
actatatata	catagagggt	acctacctcq	gctcgttccg	catccgaaaa	caqqqqqaac	540
actacytety	cacagagogo				22222222	600
tetetgegee	cgggaatatg	teegeggegg	tattctttcg	agagegaete	Caaaacyaya	
gagt						604
gage						

- (2) INFORMATION FOR SEQ ID NO:187
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...620
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187

gccaataatt	ataaaattca	aacagcctaa	acattcttaa	tgcgatgaca	ctagtaacaa	60
		aaaattacag				120
		aaaataagaa				180
tttgcacgaa	ttaagcgtag	attgatagat	aaaacagcaa	caacaaaaca	agaccaataa	240
acccagctca	gcaagagcgt	tcacaaactg	attgtgtgag	aaaactcgca	tgccgtcttc	300
tgaaaattac	gctcaacaac	ttgagtatac	ccctgtccca	acaaaattca	taaatattac	360
cctcactcca	tccttctatc	ccattcaccc	aaaagaagta	cgtccagatc	cttttaaatc	420
cattccttct	gcagaagcat	tgtatgcaca	ttgcgcccag	ttatccttgc	ctgaaactgc	480
tcgtggtatt	tagaaataaa	caggagcaca	ccaactaagc	ctatcaaaaa	tgaaaattac	540
caagtgatga	tagtaattta	cgaggagcat	tagataccag	agcacagaca	taaccagctg	600
tacgacatag	cctgaaacag					620

- (2) INFORMATION FOR SEQ ID NO:188
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...630
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188

gtccgttttg	acaggtattt	ggggagaaga	aaaccccaac	gaaacgggat	gtttaaccat	60
tctattggat	catgcctatc	gggaaatcta	cccaagatat	agtacacatt	gtgagtttat	120
agagtttccg	ggtaaaattg	ctctccgtac	gattcccttt	gcgggaagat	ggcggaaggc	180
aaaagtgtat	gtcgcatcaa	aaatgacatc	ctacaggaaa	gaagaaataa	gaggttgatt	240
tataggcatt	atatcttgag	gaaagaaagc	tcaaaatgct	cctgaaacaa	actaatagtt	300
cggtcaaacc	aaactatata	ctttggtgaa	actaaactat	atatttggtt	gaactaaact	360
atatactttg	gtcgaaccaa	actatatact	ttataaagcc	aaactatata	ctttggtttg	420
gccatggttt	tcagcctctg	ttcaatgtcc	aaaagggagt	tggggaaacg	atacaatttc	480
cttctaagtg	ctctaaaaca	atcacttctg	tctttcgtaa	ttatgctgat	agggattatg	540
gctttcggct	tttcttttgg	aagattggcc	gagataggga	cgggagggaa	agcatccgat	600



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...539
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

ggteegetga cattegget	a ttctaccacc	tatatatatg	attttgcacg	gatagtaagc	60
gtgctctgat cggtacgct	c tecacqqaet	ggacgcgcgt	cctttccgct	ttgccactat	120
catggagtac aatatggag	ra cooocaaoco	gatacgetta	tcactcgcga	tecttecate	180
gacgcaatcc agtataacc	c dacddcaaac	atctgatcgt	aatgggttcg	gcagatgctt	240
toggoatata ggactgaac	c tgaaatcggg	agtcactccc	aattcttacg	acaacaattc	300
ttcctgttcg atctctcca	ac acggaaagca	acageettga	ccagaatttc	aaccccagtg	360
tateggeagg gagattega	ac agaaaaaaca	acactattac	ttcagggctg	aaaacggatc	420
gcgcaagcag ctctatcgg	nt togatotgaa	aacccttgag	atcagtcaga	ttcagaccgg	480
agaggatgg agtacaatc	a ttegatataa	cagetgataa	tggtgctgtc	tggtacagc	539

- (2) INFORMATION FOR SEQ ID NO:190
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...680
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190

gcataatgat gagcagcaac gagaggctcg ctggccgaac gataggttcg atcttcggat 60 gaatctgaaa gaggacctcg caaatcctct tcaaagcgat tcaggtgatc cgcaacgatg 120

aataataaag aatagaaaat caaatacata gataaatgaa gaagacaatc ttccaacaac 180 tatttctgtc tgtttggccc ttacagtggc cttgccttgt tcggctcagt ctcctgaaac 240 gagtgtaagg agtttactct tgagcaactg atgcccggag gaaaagagtt ttatactttt 300 accccgaata cgtggtcggt ttgcaatgga tgggagacaa ttagtcttta tcgagggtga 360 tgatttagtt tttaataagg cgaatggcaa atggctcaga cgaccagatt ttctgctgcc 420 gateteaatg caeteatgee gagggatgea aattteagae gaetgatget tteeetteat 480 teegeacact gatgeeggae ggggaetggt egttetattt acceaaggag gattagtega 540 ttogatatgo ttgotogaaa ggtgacttat ottttogata coaatgagag acggottott 600 tggattttct cctgtgggag accgtgttgc ctatgtcgaa accataacct ttacattgct 660 cgtgaggtaa attgggagaa 680

(2) INFORMATION FOR SEQ ID NO:191

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1046 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1046
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191

gcttcggttt gctcggtctg tgcagagata agagagccgg ttcctgtatg cagaataggc 60 gcaatccgat attaaccgac atttcctgcc ttttgagaga aaacttctgc cacgatcatg 120 ttacgttttc acaaaagtgg cgatgaaggt gacaaaatag catgccgaac agcattcgaa 180 tgacttttgg tctaattctg ccccatcggc acggtggcac tgtatttgta gcctcttaca 240 agcaagattt acagcccgta aaaacggatt cggacgatgc ccaaaggagt attcggcgga 300 cccttcatac tttatactat aaaccettcc gactttatac ttaaaccetc caccetttat 360 actataaacc cataccactt tatactataa accataccac tttatactat aaacccatac 420 cactttatac tataaagcct catactttat agtataaagc ctgcgagctt tatagtcgga 480 agtattaaag gatgattgtc gtgctacact tgtgcaagaa aaaggatcag aacggatagc 540 tactgcaatg tgccaagcga aattggaaga aaggtttggg cgtgtgatgc ccatttgtaa 600 cgccctgtct gctgaggatc gtaggctttc agtccggatc cagccgcaca aggaaataat 660 cgaagtcgag acgaagcccc agaccgaggc caaagctatt tccttgtaga agcgatcgaa 720 acgaaagaga ccgtctcctg attctcatac tcctttatcg tccagacatt gccggcatcg 780 acaaagctgc tgcgcgaaac ttccagaaca gctttgtcct gtattcgaca ttcgatccag 840 acgaatatca cccatctgat cgaagaaggt cttgtccgga gtatcttcat actccccggg 900 ccgagggtac ggacactcca gccgcgaacg cgttcgatcc tccggcaaag taacgtaact 960 aaagggtata tggcgagcat gccataaggg aaagccagtc cgaaacccag attgcagtgc 1020 caaagtattg ccttttcgag agaacg 1046

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 577 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...577
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

60 gggcctcaac aatcgaataa aacggcattt gagaatgatc ttttctcttt tcttccgtgc 120 cggagcaaga gttgcataca aggactaaag ataattgcgc atacagagtc catcgggcag attggagccg gaaatcaaga tcgttcaatg cctgcgaagc agatcgagag aattacggtg 180 240 ttctatacqg atggcactat caagagtttc gctcaaacaa agagtaagcc tctctttttt cgtaatttgc actcgaatac tgcaactcga tttctcgatg aaatacaacc ataactgcgt 300 gtcgcgacca atacgaagct aaacgacagc tatttccttc ttaacttgta ccggagcata 360 atgaagtacg attatctctg ccggaaataa agccggacag tttgttcagg tactgactgg 420 atgtccaagg ggcttttttg ctcggcctat ctctgtttgt gatgtcgatt acgaacggca 480 540 ggaactattc ttctggttca aaaagtaggc aagggtacac gtgctatagc tacattacag 577 catecgatte attggatett etatateege ttggaca

- (2) INFORMATION FOR SEQ ID NO:193
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...515
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

60 teeggettet tegaactget tggcaaagte cacceaegaa teggagegga geagttgatg 120 ctggctatta cggggatagc cacctcgcgc ttcacttccg gaggaagtcg aggtgtttgg 180 agatotogtt gototgtaca taggoatgat atagtotgoo gootoaggat aatocatogg 240 ggacatcatt tgggactttc tgcctcgatc tgctcttcga acagtgattt cagtacgatg 300 gcagcacacc cgctgcttcg agatctttga tggttttgag gttgcgggtc agtccgaact 360 tgctgcaaca ataggatttt tcaggcgcaa gccggcgaac tcatggacaa atcgatcata 420 totgtttatt atgaattacg aaaaagaccc tgaagccttc cccgatcact ctcggccatc 480 totytttaag acagacgaaa aacgoootog acaacaaggo ttoocagtgo otooggoaca 515 tatatgcgag tgcgggctac acagaaggtc tattc

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 962 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...962
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

gggccatgag tttgtccgta aaagaggcga agtagtcatc cggcacagat agtgtcgaat 60 actgtcctct ttcggacgga tattcacatc ggggtcgact gtttcatgtg agctttgtta 120 gttacgatta tagaggcttg ttcttaggca agtttaatca tcgggcgaca aaaaacgctc 180 caacttette acageaggtg ggaccaatge ettgagagea eetteegagg taceggtgat 240 ttcggcattt tttcgtaagg catctcatcg tagtaccgaa ggttgaacac caacgctgtt 300 tatcaggcaa ttccagtata gccttttgga aggtaatctc ggctcatctc catcgaaata 360 aacatccccc gtgaggttgt cgagcagata gggttttcgt ccgtgatcga tatactcata 420 tegtettega tettttett eteaggaaat tgagtgatte gtacatgget ateegataga 480 gccaggtgga agtttggcct ccccacgaaa accgtccaat gcactccatg ccttcataag 540 gtattttgga gcaagtcgtc cgtatcgtca tgactgagca ccattcgggg atttgccagt 600 agagtttacg gttgtacagg cgtactacct tttcaaagcc atacgccgcc ttgccggatc 660 tetcagetet tecageaact ettettegaa ateaataget tatcageeat aatgatgegg 720 taaagatagc aaaaggtgct ttatctatgt caataaagtc gaagattcag ctctgatcct 780 gtaggagaga ccgaaacatg agagagttat gctcctgtgc tttccattct atgccgactc 840 tatcctttcg gctcatgcgg caatccaaat tcaaatcctt tgagttgcgc tactcagaca 900 aggtattgca aatgeetete ggetattaee caaataegtg egaaaaaagt ttteaacaae 960 ta 962

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 599 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

ggcgaagagc	atgttcgggc	gtacgctcca	gtcctgagct	ttgccgtccg	aacgtaatcg	. 60
			tcggggaaga			120
			ttctcgttcg			180
			cgggggatga			240
			ctaagacgta			300
			ataagatacc			360
			cggcatactg			420
aaatcccaac	gtccggttca	tcagcccgtg	tatggtgtcg	tcatcttcat	gcagtcgcat	480
gtagcgttcc	tcgccggaat	gacggtattg	acgatgccgt	tcgaatcgct	tccggtgctc	540
tacacaccag						599

(2) INFORMATION FOR SEQ ID NO:196

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...561
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196

gctgcccata	cccgcagcca	aaacaaaaag	tgtgggtttc	atcggtttca	aaaactcttt	60
tttatatgta	atgctgcaaa	gttacgatta	tccacaaagg	atcagccgaa	actgtacagg	120
ttttcatatc	tctgcacagt	ttcggctcta	tatcttttca	ttaggggata	ctccgaaatg	180
ctattcctta	ttgctttgca	aaaaaggaaa	cagctgctat	cacgagcaac	gtgaacgggc	240
cataatttga	gcttgtcaag	gatttgtttg	tgtttgaggc	tgcatcgctc	ttctctgcat	300
cgaaaacgat	ttgcagcttt	ttgtgatcaa	gaatacggta	gattctgtca	taagcatatt	360
cgccaaaagg	gttaaggatg	aaaggagtca	tttccttttt	tccattcttt	tagagaacgc	420
			gactaagccg			480
agattgatca	cgcatatcgc	attcggccga	gtgccgtatt	gatgcttact	ccggtagcac	540
tgcaatctct	cggagctcat	g				561

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 655 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...655
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

cagtattgcc caatgggttg atgagcgtta cccctttcaa tgtcagcggt cgacagagaa 60 tegettegae aaagattege gttggtggag tgegeetttt eggeegaeaa tagttaetge 120 ateggtttea gecatgtgaa tetgagtgag taggetgtee egaaetgagt ggaataetge 180 tgatggccac ttccggacat tcgatcctga ttactgctgc tatggctctt cgctcagtcg 240 300 agaattgcgc gcccgggaga atacaaggct gtattggaca aatacggtat agatcagccg tgaccgtaac cgagcggact gctttgaccg aatttgcttt tccgaaggag aaggccatat 360 420 cctgctgaac ctgggacagg ccctaagcaa tgatcgggag cctctgttcg attcttaaac gactccacag tegteggeag eggetgatgg ggacgttetg etacaateeg caageagttt 480 ttcgtcagta ttcgtacttc aggtgagtcg gcgaccgatc tctgccggct attggaagag 540 cagcetecta tgacagtgga ageceaatgg gattegactg cagggaaaat ageagtaega 600 eggetacage gtgagatgag egtgatgaca tegtgtegat etegteaact ggate 655

- (2) INFORMATION FOR SEQ ID NO:198
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 694 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...694
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198

tgtcgagagc atgatctgcc ttatacggaa accaaacatt tcgacgaagg gtgatcaaca 60 actgcgacat tetetacatg acacgagtae aacgtgaggg tttacggate tggaggaata 120 tgaacgggtc aaagatgtct atgtgctacc aacgctatgc tgtccgacag ccgtccgaat 180 ctgcgcgtac tgcatcgcta cctcgtgtgg gggagattgc ctatgatgtg gatgacaatc 240 ccaaacctac tttatccggc aagcactgaa cgggctttat acgaggcagt ccatatttgt 300 360 gaagtgctcg gcatagacgt tgcaaactaa gcagatattg taagaaaaag gaagaaatgc tegtegeege gattagaaac ggeategtga taaccatate eeceegaega aactgtteaa 420 ggtggctact ctcctgcaac tgatgatttg gacaagcgga tcaccatcgg caacaatttg 480 cgcagtcgga ccatggttcg aaaggagtta tcaagataga ggacaagact ttcgaagaga 540 ggaattgaac cgcatcgctc ttattgcccc gaatgtgcgc ctgaacatat tcgggactat 600 gaagttgtag aaaaacgtca ggtggaagta ccacacggat tgtgggtctc gtccgttgtc 660 cgaatccgaa gtgtattacg aacaacaacc gatg 694

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...434
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199

aggactasta	gaatatgttt	ttcccgaact	cttagccctc	aaaggagcaa	aacgcgtgat	60
ggggccgac	ataaggagaa	tctcactcat	acttataagt	agtggacaac	ttggctcggc	120
ageaccagae	tetttagete	aggtaggagc	attgctacac	gacataggca	aaccacgcac	180
teagegatag	attaccascs	gtggacattt	cataatcaca	actttgtcgg	agccaagatg	240
taaaaagttt	attanagaa	ctccaacttc	cgctggatgc	caaactcaaa	tacqacaaaa	300
etacetetet	ctccaaacga	atcoagacaac	tetggtggae	gaagagttac	ggattetgee	360
actegragat	tratattage	anagagatan	tgtatagatg	atctgatgat	gctatgcgaa	420
		aageeggega	cycacagacy	accegacyac	gg	434
gctgacatta	caag		•			

- (2) INFORMATION FOR SEQ ID NO:200
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 900 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...900
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

attgagggag ggt	tagttett teegeeatet	ggactgtctg	gccctacagg	aacgcgattc	60
gtattccgtc ato	ctgaaac gggagatac	caggaataaa	gttgcctttg	cccaaactct	120
ttcgccgcct gat	tacatete gaagaagead	tgcagcagac	caaacaatat	caaagacaaa	180
aaaacgttcc aas	atagtage tgactaatti	: taataatcca	acatataata	atgacaaaca	240
agaacacaga aad	cagcaaat ggacggtago	tttagcccta	ctgtttctct	ctatttgccc	300
atcggggcat cto	gctcagat tatcaaggat	gtagtcgttt	ggaaacctct	cttcaggata	360
gegacaegee tgs	agaaaaca ttggtgttta	a cgccacgatc	aaacccggat	ggcaccttta	420

tgaccaaaat ctgcccgagg aggccctaca tccacagaat tcctgttcga taaaatgacg 480 ggagccaaac tgtcggtaag gctattcctg acaaagctcc tgtcaaccga tacgacaaga 540 gttcgaaatg gatctgagat ggtacgagaa gactgtctct ttccgtcaaa aattcaggtg 600 acggaccctg ccaaattctc tatcaaaggt ggtgttcctt catggcttgt aatgatgaaa 660 actgtctgcc acccgaaacg agcgactctc tttcgatgct tcgatgatca agagcaaggc 720 tgcagctcct gatacgaage tgaagctgct gaagcggttg ctgccgagac cgcagcggat 780 actaatcgca gaccgatget geegaagete tttegteeaa ggetgaettg tggeaceggt 840 tgttagegag ttgegtgeat aeggtgatga taegeteaag eageagaaga gtgeteegtg 900

(2) INFORMATION FOR SEQ ID NO:201

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1120
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201

aacaacttgg atctgcageg caacaagatt cagetetact gcaatcaggt taegtcaceg 60 atgaagtaca gggtatcgtg ccggacttcc tcaccctctg cacggggtca tcgattcgcc 120 ggatattccc ctcaacgtat cgcgctctat ctgcagagcg atgccaatgt gaagaagatc 180 togtotoata toaccagaag gtggcagaco gtotggaaga aattttcaaa aacgacogco 240 ccacatcgag gagaaatggg atagtctgaa gctcttcgtc gaatacggta tgctacggat 300 gagaagttet atgagegtge agecaaatte tteettttea eegtatggae ggacacaagt 360 acacgttcga cgaataccga acgctcgtcg aagtgtacag acggataagg acggacaggt 420 agtgtatete tatgetaegg aaageatgga eagtaeagee aegtgaaaeg tgeateegae 480 aaaggctaca cgtgatgctg ttggatggtc aagttggatc cgcatatcgt gagcctgctg 540 agcaaaagtt ggagaagaca cactttgtcc gtgtcgatag cgatacgaca acaatctgat 600 ccgcaaggag gaaagagccg aagtgaaact gtccgatcgg agcgcgccac tctcgtgaag 660 ctgttcgaag cacgcctgcc acgggagaga agaagcactt caatgtagct ttcgaatcgc 720 teggageega aggtgageea teettateae acaageegaa tteatgegee gtatgegega 780 tatgcacage tgcageeggg aatgagette taeggegaae teeeegatte gtaaatetgg 840 tacttaatac cgatcatccg ctcatcgaca gggtactctc cgtgagaaag aatcggtaga 900 gccttcgctc acagagctta gagcgaaaat cccgagctga aagcggaaga ggccaagctg 960 ctcgatgagg aaaaagggaa aaaccggagg aaatccctgt tgccacgaag gaagccaagg 1020 agaacaacge gtegaacagg ecaaaacega aggeagtate aacgateaac tgaccaaaat 1080 gctcaggaca acgagctgat aggtcagctc atcgacttgg 1120

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1540
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202

60 accatatate getatgaaat taateeaagt teaaatteat tetteeggag gaaetgattg 120 cattagagee gaccaagtte egegacgaat egegaatgtg gtegtacate gtegtacagg 180 agaaatcgaa catcgcgttt tcaaggaatt ctggagtatt tcgacaaggg tgataccttc 240 gtottoaaca ataccotgtt tttootgooc gtototatgg taataaagag aaaaccggtg 300 ctcagtcgaa gttttcctcc tgcgtgaact gaatgaacga ctgaagctgt gggagtcctc 360 gtggatccgg cccgcaaaat acgcataggc aataagctct attcggcaat gatgaagagc 420 tggtggcaga ggtgatagac aatactacct ccgagggcgt acgctgcgct tcctgtacga 480 tggctctcat gacgaattca agaactgctt ttccaattgg gacagactcc tctgccgaag 540 tacatogato ggaogtgaao aaagaggato oggagaggta toaaagcata tttgocaaat ggaaggegee gtggtggeae etgetgeeag tetteattte ageegegaet gatgaaaega 600 660 ctggagatca aggactgcca tttctcttac ataacggaca ccacgctttg ggagcttatc 720 gcgacatcga tgtagaagat ctgacaagca caaaatggat agcgaggaga tgtatatcac 780 ggaggagtcg tgcataacat caaccgttca tgggacgaag aaaagaagat ctgcgccgta 840 ggaattegat tettegtget ttggaaacag etgtgageae agaeggteat eteageegtt 900 cqaaqqttqq accaatcgct tcatctttcc tccatacgag ttcatctgcc ttctgctttg gttacgaact tecatatgee getetetace caetgatgat gaeggeeget tteggaggae 960 1020 atgaactgat tatgagtgca acgacctcgc tgtaaaagaa aagtatcgtt tcggtgctta 1080 tggtgatgca tgctcatcat cgattgagta tggccatagt gtatctttct ttgggcaaca 1140 acttaggcga tcgacacagt ttgttgtntg cagcattgga gatgctaaaa cgagggtggg 1200 cagactgctc accetttete ggttetatga aaccgaeegt ggggattega ategeeceat cctttcctca atgcggtggt ggcttgcgat cggaactcaa accacaggac attctgcaca 1260 1320 tcacacaagc catcaaaggg aattgggtcg tacacaaaaa agcaatggag gggtctatca 1380 cgacgtccga tagatataga cattctattg cattccgtat acccgaaagt acgtcacctg 1440 agctggaact gccccaccca caaatgtggc aacgggattt ttgcgtatgc cgctatcgga 1500 cgtagctcct tggctgcatc cggaggctcc actccgaacc tctgactaat gaaagaaatg 1540 aatgtaaacg acttcgagaa atggctccag tcggttcgta

- (2) INFORMATION FOR SEQ ID NO:203
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 656 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203

cgcaattgat cgggatggct attctgattc ttctcgttct ctatgccaag gcaatgactt 60 geteaggget tttegetgae agaeegetat gatteggagg agaettaeee ceacaaette 120 gaggagaaag tgggtttcga tgagattgtc gccttctcat cggccattgc catagtccga 180 tgggcagcga tcgggtatac agatgcatgc tcttgcaagg cataacgaag tcagccgctt 240 gettgegaga eggaagaaat geanattate etgagagaag aegaettgtt teceatetee 300 gtctggccga tgtgcgagaa gcactaaacc gtatccgacc tgcggtacct atctggaaga 360 gegagagttg caggatgtgg ctactgetet gagacaateg aggeteteat cegtttette 420 catgtggggg aagaagagga ggtaaggata caccgtaccc ccacctccaa actctttgt 480 eegaggteat geettteegg atetggagaa gegtateage agettgtteg ateggttegg 540 aaaatgaaag acaatgcctc gcccgaactg atgaatatcc gtcgcgaatc tcttccatag 600 agaaaaatat ctcgcgcact ctccaaggca tccttcgttg gctcagtccg aaagct 656

(2) INFORMATION FOR SEQ ID NO:204

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 919 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...919
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

cagcaaagca aatgctagat aaggataagc ctcggactta gcaaagcaac cagtaaaata 60 ctcactgatt ttgatcgctc ctcctgcgga tcgatagctt cagaaagccc gaaacacgaa 120 ggtcagacct aatatgattc gagaaagtca gcaaggaaac gtttcatccg ttcaactgta 180 tcaatgcgaa gatggctagt tgatcatatc catgtagttg gcatccaccc cttcggatat 240 atatgateae eteegagate ttetatetet ttagtgegaa atacettagt cagateaagt 300 cggcaaagga tgacacacgc atctgtctcc acgcctctcc atatcatgat tcttatcaag 360 catcagogac atggottcac gaatottgag gtatacaggo gcagagotto ctotgtotoc 420 atcttaggtg tgtcagctac tccagctcca attggatgag agctattact ccataattga 480 cgacacctat aactcagact ccactccttc atccacctta ctcaaacctt tcatctgaaa 540 tttcgaatgc ggttggcctt gatataaagc tgatcggtca gagacgacga cgcatcactc 600 gccacgaggc tccatagtcg tgcagttttt tctgaaaacc tcacgacaaa tatcaatcac 660 gtgctcgaac tgctctactg tatttgcttg gctgtagtca tttctttctt tgcttcttct 720 ccgttttttc cacttttcgg ttttctcctc ctcggtcttc ttgccaaagg aatatatatc 780 ggtgtatcga tgactttctc ttcgagcaaa gcttctttca acaccctcgt taagttggac 840 acatagtgga acttcaagcc cttcagatag atatcgntaa tcctctatgt ccttgcgatt 900 ctcttcgcac aggatattt 919

(2) INFORMATION FOR SEQ ID NO:205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1055
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

60 cgggggattt tectectett tttgggette tgccagcaat gagggattta ggctatgece aatcccacac tgccgtaccc ggtcacactc gctgacgagg ttatcagggt cgttgcgtgc 120 ggatgettae cegaceeggg atcaaggata eggcatgggt agttatetgg tggeggeate 180 gcttttttcc ggtaagtcga tgtatcgaaa ctgatctctg ccccattgga agccacttac 240 ttcggcacag agtacgccag cgtccgattc ggctgcgagg ttactatcga tacaggccgg 300 aagcaaatat atcgatggca gcatagggcc ggatgccgtg ctgaaggcaa agaccaatgc 360 acgategeeg gegtatteta tgaagtaact gagataegee etaettgaat ggcaagaace 420 480 totatactgc acceptocato gatotattgc caaagtgata gcaaatgata cggatgggtg geageegtte ateteaegtt eegateegtt ggeaataaag tegtggaett ggeeaacaae 540 600 agtaccgctt ggctctggtc ttttcgtctt catcgcgtgg agacgagtta tcggctccgt 660 ggatagcgaa ctgcttgtcg atgaagtaac ccttacgtga ctactttacc cgaataaacg 720 ttatgaaccg gcgatatttt cttttgatgc ttgcttttgg agcctctgct tcatcctgtc 780 ggctcaggag tcgaagcttc tgtccggccg tcgctttggg agttttccag cagagtgggt 840 atgctgtggg agcatccaca ccggtacccg taccccaagc catggagcac gtcacgcgtg 900 gtatccgcga ctgaatccga tggtgcaact gagtgcttcg cgcgtttgct tgccggcagt 960 ccgtgggctg tgaacgtggg tatagccgta ggaaaaaagg catggaagct actacacgag 1020 tgaaagatat gaaagtaget tegtgtegga etegeettat geeeggeaac eetgatgaag 1055 aatatccgga ctattcaccg gcgacaacaa tacgg

- (2) INFORMATION FOR SEQ ID NO:206
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...522
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206

cgtgccgttt	cttttgccca	acgggacaac	tgctcgaaag	cgtcagaaat	getegeeteg	60
caatttgcga	cacagccatc	caaagaacta	acggatttcc	ttaccccctt	ccctttcttt	, 120
caactgaaca	aatcgatcta	ttcaaataaa	tgacagattc	tttcgacaac	gaacaaccgg	180
atatagagtc	atctgttccg	atctgcttcc	cgaagccggt	aatcgcctgc	cggttgatca	240
tectgeatgg	ctacacacca	tctcgggggc	atgtatcgaa	actggtatct	cgatatgctt	300
cttacgtaat	tctggagcgt	gccgtgcccc	atatagaaga	tggctcaagc	ccatacaaca	360
ccgtatcctc	tacaccatge	accattggtt	cgcaatggtc	ggtatgaaca	aggtagggaa	420
ggtgaceggg	acagactatg	gttctacacc	cgcacgggag	atgcttctat	caacgatgct	480
cttcgtacag	tggggcaaaa	agggctattc	tgatccgaaa	cg		522

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...579
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

```
cccctgccga ttatcgcggt gagataggga ttattatgat caatctctca atactccttt
                                                                        60
taccatagca gatggcgaac ggatttgcca gcttgttacg ccagacatga acaggccgaa
                                                                       120
tgggtgctta cagacgaatt ggccgatcgg aacgaggtgc aggcggattt ggtcatacgg
                                                                       180
gcaaagaata attttcatct cccttcaact accacagatg cggatccatt ctatcattct
                                                                       240
cctgcgtttc ttttagttat ttctcctgta gccggaagta tatccattac agacgtacag
                                                                       300
catctaagtt cgaccgatat ttctatgaag gtgtccggca gcggaacagg agaattatgc
                                                                       360
tgcagettte gacatettte getattgeca tegttgaate ecaacgatge ggetetggta
                                                                       420
toggagttgg gaaaactgga ttttgccatt gggcgtcagg aggaaggaac cooggtattt
                                                                       480
ggaacaaagc tatcggctct atccgaccac caaggaacta tggcaatata ttaaggtgcg
                                                                       540
ggtatgaacg ccagggacga gctgacgatg ctgcaggct
                                                                       579
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 578 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208

tcccccatag aaatctcaaa caaccgcaaa gtctttctga ccaatcaata ggggttgtaa 60 acatcactga cgggatggaa cctccgatta ttgccggatc tctgcttcct atggatcttc 120 cgtccgggtg tatggtcatg tctcacacgg tgggacatca taggccattg ctatttggat 180 atctacccaa ccaattctat ccgctcagca cgaaacccgt tgcaggagac gatgaggttt 240 ttgtcaacaa caaggcaggc aaatagagat cgatagcaac agccccatag tccagtggtc 300 gtatacgatc ttgaggggaa aagtgttttt cqcaaaagaa tgacgaaaac gcttataccc 360 tateetttag ageaeceatg eteggettta tgeeateatg ategaaacae aaaattegat 420 tatcaataaa aaacttaatg tacacagcta tgaaacgaat aattttatta ctcagtactc 480 tetgettett gtateacett atgtacaage geagaatgaa ggtteagatg ettattatea 540 caaatgtttg aactaatccg ttccgacttt cgaacgga 578

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 996 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...996
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209

						
			attttttatt			60
			tcattagcaa			120
			tgcgaggctt			180
			actttcgcat			240
agttttagtt	caaggctcct	tcttgtccgg	ggatgagaca	aagctccaat	tttgaccctt	300
			tctgcgagcc			360
tattctatcc	ccctttcgat	aaagttttt	tcgttgtcga	agcagttttc	tttacaaacc	420
			gagcttcggt			480
			atgatgggcg			540
			gttttgtatt			600
			ggagaagtct			660
			tgtctcgtaa			720
			aattgtggca			780
			ttttctgtat			840
			gtaataatat			900
tcgagggaca	agggtccccg	atattgaaga	acgagtgatg	catccttttt	caacaaaagt	960
gttgatgcct	aaaaagccaa	aagtaacgtg	ataggc		_	996

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 551 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...551
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210

actctagagg	atccccggaa	tgataaagcc	gacgggatta	cgaggctttc	cgctttttct	60
		cagggccgtg				120
		tttttgattc				180
		aatgttcact				240
		tcggtaaaag				300
		ttgtgaccag				360
		gctgcaaatt				420
		caatgataat				480
		ttacatctgc				540
gaatttggat		·				551

- (2) INFORMATION FOR SEQ ID NO:211
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...633
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211

atccccgaga	attcgcttcg	acaaaagctc	tgatgctaaa	aatcaagcat	agcgacaaga	60
gaatacagcg	aacaggataa	gatgaatatg	aacttcttct	tgacataaca	tctgttggtg	120
tcagcaaatc	ttttgtttat	aaagatgatt	aaatttagga	acaaagtact	ttaaacatat	180
cactgacgac	gagaaaagag	gagggtaaag	ctattcttag	aagcaactcg	aataatgaat	240

gactagcaaa	ccaagctcgt	aatgcagttt	gtggtgagcc	agaaaaagta	ttgacgtttt	300
tgatgataga	ctgagcagga	aagcctgtcg	ttactatacc	gtagtgaaaa	ggagcaggca	360
aacattataa	aagaacttga	tcagtaccaa	gtaaatattt	tgtaggggat	gatgcttcag	. 420
attatagcgt	agccgatgct	ttcgtgatgc	gatgaattac	cttgataagg	caacacttgt	480
cgattttgca	aggggcgaaa	gagataatga	cttttgcaga	agccttcgag	tgcaaggaaa	540
agaacctcaa	gagaaaaaat	ctaaaaaagg	gaaagacaag	gccacttcgc	tcagaatctc	600
tttgcagaac	accagatgat	caataaagaa	tcg			633

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...561
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212

gagaatccaa aagcgtaata gaaaggtata caagcaaaat taggcttcac ggagttggtc 60 ttttttctta catttgtgga ctcaacaact aaatgcccat atatgctacg acttcatata 120 acategacaa acagtaagge egatttteta teccacatae ecaeteteee ategegaaag 180 gagagaaaag aacgctatac ctatgacgaa caagcaggaa taaggctatc aatagccgga 240 300 caaaacataa ggcacgcacc cgattcgagg ctgaatcagg tgcgtgcctt tctttatcgc 360 ctgtcgaaag ggctttcttc atctacgatc tatatataaa tggatgacaa tctatataga tatggaaatc gatttatata taaattgaaa acattaatat acagatcgaa aatgatttat 420 atataaatcg aaaatggttg aatacaaatc gtttttccat ttcttagaaa cccgaatccg 480 agctaaagaa ttcgttttac caccttttgg gggttcaaaa agctcttact ttcaggtgct 540 atttagaatc attcaaaact c 561

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 676 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213

tgctgtcatc ttgtgccaag gatacgccgg atgcgcccga acagtacgca tcactatccg 60 tgccaaacta ccggaaggca gtacgataga gagtctcgag gtatagccat cgaattcctc 120 gatettegta eccaacagaa agtggaaaac agetegacaa ageeggtgtt tgetetetta 180 gtctggatgc cagtgttata cgattacgat acgtggcgaa atagggaaca acagtatcgt 240 tgccacaagg aaaactattc catcgcagag aatactacct tggagcttcc actcttgtga 300 egaagateeg eeetteeggt etgetgttea aagaagtatt tttaatggag agaeeaacaa 360 egggeagatg atgeaceegg ateagtaett egeatataea ataatagega taaggtggte 420 tatgccgatg gtgtcgcttt cgtcttgccg cacatgccaa cgtaacaggt gaagacgctt 480 tcaccgagga ttgaccaaga acaaccgcat cgtcctttcc atgatctata ccattcccgc 540 aacggttcgc agtatcccat ccaacccggt ggtcagctcg tgatagccga acggccatca 600 atcaccacga tgccgagcat ccgaattccg tggacttagc ggtgccgatt tggaagtcta 660 tgagccggat cagccc 676

(2) INFORMATION FOR SEQ ID NO:214

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...294
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214

ggcttggttg	tgatctcatc	aagacccaat	tcgtcaagag	ccttttcggc	aaaccgttgt	60
gataatcgat	cagatettee	acgatcggac	gaatccccga	cgattataaa	tacctgtcac	120
agctcggatc	ttttcttcac	actgcactcc	ggcatcaaaa	gggattctct	gaggagattc	180
aattcctctc	cctgagcatc	tcaagggctt	tgatcagaag	catcgtcttt	ttattacaag	240
ctatacatcg	ccgattttct	tgccgangat	aatgggatcg	ccatatacat	cqaa	294

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 623 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...623
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215

gettetgete caaaagggag ageegggega etgeaceate aceatetgea tageegtace 60 cctaacatca aagaggtatg tctgacggcc gacattatat tgcagctttg gggcagcccg 120 aattootgac agoogatatg gtaaagoogg agotgtagta gtggacgtag gtaccaogot 180 tgtaccggac tcgacagcaa aagcggtttc cgtctgacgg gcgacgtcaa attcgatgaa 240 gtggccccaa gtgctcgtac atcactcccg taccgggcgg agtaggtccg atgacatcgt 300 ategeteatg tecaatacee ttetggeaag taaaggattg taeggtaaac ceteetteee 360 ttatttgcca acgaccttat cgaagaggcc cgcatcaata tcggttcgtc cggtatgatg 420 atcggcctct tttcttattg aagtgtgtca tcatgcgcaa attgctgcgt tgcttgcggc 480 attogtttct agcgccttgn actttacgca ttcttaccca cctaaaatgg ggtatgccaa 540 accgaatttt gacacgggct ccctcctgcc gatactttca agaattcgtt cgtatccttt 600 ccgttaggag gtaaaggcgt act 623

(2) INFORMATION FOR SEQ ID NO:216

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...381
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216

ggccaaaaaa	ctctgtgctg	tagttgttcg	gcttccatcc	ttccaacttt	gccgatatgt	60
			cgcttcgacg			120
			gttgcagata			180
			tatatcccat			240
			cctcttgatc			300
			gtcccacaca			360
tgattgctgc			-	•	•	381

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1957
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217

```
ccgtggtcgt aatcatcgtg gtatgatatt ttgcgcggcc aaaattagca atactatggc
                                                                        60
cgaacatgct cttttctgaa gtgtactgat cccattctga tgttaaaaaat cggattttct
                                                                       120
taccattagt gtcctaaaag ctattttgca aaagattagg agaggtactt cacagcacct
                                                                       180
ctectttegt etattacaga gecaectaag gtaaateate ttacettggg tatattecae
                                                                       240
aaaaaactct gatgagtaca aatataagcc tattcgccca agttatccgc ctgtgcctcg
                                                                       300
tecattgatt aagaagetet etacagagtt teaggtagae aagacageaa geattteace
                                                                       360
tcatggcagc acttagtgag catgattttc agcaattctc aagctgtatc tccttacgcg
                                                                       420
agattagtaa tggcttacgc tagccacagg taacctcaac cacttaggca tatgcacagc
                                                                       480
accetetaag ceaatttate ttateagaae gageacegta ceteagaett etttegaget
                                                                       540
getattatge ettgetagat tattteggae ageagggtat ggggeaagge gtaagttteg
                                                                       600
ttttaagcaa cccgtcaagc ttctagactc tacgacctta ccctttgcct tgccctatac
                                                                       660
gattgggcta aatacacaca tacgaaggag ctgttaagct tcatacactc ttagacttca
                                                                       720
agactetgtt geetgatatg tgeatattag tgatggtaaa ggaeatgatg geaagatgge
                                                                       780
caatctattc ctatcccagc aggaagtatc gtcgtggctg accgtggcta tgcgataccg
                                                                       840
cettgeteaa tagttgggae ageacceaag tgagttttgt agacgeeace caaggteett
                                                                       900
aaaatatgag gttattcaag agttggaact ccagaacatg ggcatcagca aatactcgta
                                                                       960
gatcagagag tacggctcac ggcgttcaga cgcaaggcaa gtacactaag ccattgaggc
                                                                      1020
atattgcccc tacaacgagc aacatggcga tgtcgttgag ttattgacca acatagaccc
                                                                      1080
cttgcagcaa gtagtatagc cttgctgtat cgttcaagat ggcttatgag attttctttc
                                                                      1140
ggaatttgaa gcaacgcctc agcatgaagg cctttctgga acaacgcgca atgccgtaga
                                                                      1200
ggtgcaaata tggacggctc ttattcaatg cttttgatgg tctatctcaa gagtatcgcc
                                                                      1260
aaatateggt ggtgttgtet aatettgtet ettegetaag aateaacaca tttaccaaga
                                                                      1320
tggtctgatg caatggctta atgagccgtt tacgcctccg ccagagcccg aaatcagctc
                                                                      1380
ttttagcaca tagggggatg accacatttc gaaaaattga tgtcaggggg ctaatccgct
                                                                      1440
ccaggactaa ggatccctat gcctcaagaa aaacttttag gacactaatg attttgaaac
                                                                      1500
ccaaaaaagg catcaaggta attctgcagt cggcaagacg gttaaagtat atgtggtgct
                                                                      1560
caanntgaat cgcaggcaag gcaaaagccc ttttggcaaa tgttaatgca gcagacttga
                                                                      1620
tgctaaattc aaagaggtaa tcgaactgtc tactcaggct caagcttagg tacggtagcc
                                                                      1680
gatggcccaa atcctgctac ggcggctgga aagatgccaa aaagaatggt actactgatg
                                                                      1740
agacaatcat gatgacctgt ttgcgccttc tgatgctttg actatcgaag ctgctgtatc
                                                                      1800
cgaggccaat gcttcgcagg gattaagaat caggccaagg ttacggtgga gcgttctgta
                                                                      1860
gccgtgcgat ggtttcaacg aaagcccaga gctatgaaat taaagctact atcaaattgg
                                                                      1920
tagtattgct gctggtgatg ttttggctac cattacg
                                                                      1957
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 782 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...782
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218

aggtaagggt	cancggtctc	aaagcgggtc	actccgaagg	agagattcaa	teggtteteg	60
gcaatgccac	caagatcctg	actcgctatc	tctatgcttt	gagcacgaat	tggattggaa	120
gctctgctct	ttccagggag	gaaacctcac	aatgccattc	cgcgcgaagc	tcatgccgtt	180
atcggcctga	aggctgtcag	aaagaacgtg	cacgagttat	cttgaacgaa	cttcgctgct	240
gcagtgagga	cgaactcaag	cgagtagatc	cgggtgtgaa	gctcgaaatg	aaatggtagg	300
aaagcctgca	tatcgtatcg	attgtgacac	gaagcgtcgt	cttttcgcgc	cctgtatgct	360
tgccctcacg	gcgtctacgg	tatgagccat	gaatcgaagg	tttggtggaa	acgtcttcaa	420
acttggcttc	cgtgaagatg	aagaagatga	taagatctac	gtggagacca	gccaaagaag	480
ctcgacatcg	ctcttatcag	cgatatagcc	aatacagtgg	catccgtatt	cgagcttgcg	540
atgctaaaat	cagcttccgc	gatccgtacc	ccggatggaa	acccaatccg	attcgccgat	600
tttgaaagcg	gcatctgagt	cgtatgagcg	cattttcgtc	gtaaacctgc	tataaaagca	660
atccacgcag	gtttggagtg	tggtctttcc	tggataaata	cccctatctc	gatatggttt	720
catteggeee	tacccccgag	atgtgcactc	tcccgtagag	aagatcgaaa	tcaagacggt	780
tc						782

- (2) INFORMATION FOR SEQ ID NO:219
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...3\overline{49}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219

gtttcggcgg	ataaaatgtc	ctcgatccgc	ttcatctccc	cggcaacgaa	atgcgcgtat	60
agccctgctg	ctgttggatc	tgcaagtgct	cacgcagata	cgtccttgag	gggcttgcag	120
ccctaccaga	agatacagtt	tggagccatg	ggccgatcgg	caacgtaagc	gaccagatcg	180
gccaccgtat	gtttctcacc	tecteteege	ttgtcggaga	gatggtcctg	cctacgcgag	240
caaaggcagg	cgcaggtact	cgtatatctc	ggtcgatgtg	gctacngtac	tcctggattg	300
cggcttacta	cgcgttgctc	gatggcnatg	gcaggaggca	cacggcgat		349

- (2) INFORMATION FOR SEQ ID NO:220
 - (i) SEQUENCE CHARACTERISTICS:

142

- (A) LENGTH: 625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...625
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220

cgatcttctt ccagtatgta ggccggagat gctatgtcgt ggtattttgc atctcttagg 60 attagttctc attcggtatc agttccaaga acagctctgg agctgtgcct catcaatgac 120 agagggggcg tegateatga catecegeeg geattgttet tegggaagge gatgeagteg 180 cggatgctgt ccaaacggcg aagagcgata cccagcggtc taagcccgta agccaatccg 240 ccgtgggagg tgctccgtac ttgaaggcgt tcatcaggaa gccgaactgc tccttgcttt 300 ctccggcgta aagccgagca actcgaacat tttctgctgc aggcactgtc gtgaatacga 360 atggaaccac ctccgacttc gacaccgttg ataccatatc gtaggcattg gcacgcacgg 420 nacctggate ggtategage aagggatgte eteeggette ggaetggtga aagggtggtg 480 catggcgtag ategettegt tteetegtee cattegaaga gggggaagte caegaeceaa 540 ggcaggagaa tttattcttg tcgcgcagac cgagctgaga gcccacttga ggcgaagttc 600 gcacagttgc ttgcgcgtct tcatg 625

- (2) INFORMATION FOR SEQ ID NO:221
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 679 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...679
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221

cggagccgct tcgccggagg gaaaaagatc cgaataacgc accggatggc ataaccgaag 60
acagtgaatt gcccgcgcca tccggcaata ctgccataat ccaaggaatt ccgagagcaa 120
gagaagcacg atctatcaaa tagcgcgctc agcattgtcc gaagcatcga taataaggtt 180
gcactcgccg gccaactctc gggcattcag ctccgtaaat ctttcggtga aagcttccgg 240
acggcatcgc tattcatcgc ctgcaaacga gctactgccg caatggcttt gggcgtccca 300
aatcggcttc ggaaaagagc acttgacgtt ggagattgct gattcgacgc gatcatcatc 360

gacaacgctg	atatgcccca	cgcctgcagc	acgagatatt	gcaggacagg	gcaaccaagg	420
cctccggctc	ctatgacaag	gcatgcgaac	catctaatcg	ctgctgtcca	teggetecca	480
cttcgggaag	gccgtctggc	gagcgtaacg	ttcggaaaag	tttggtttca	tacaaatgat	. 540
cggatggagg	aaatgccgga	gggaaaaccc	catgtgcagg	ctttccctcg	aggccccaaa	600
ccattctcta	ttaatgatcg	taagaaaggg	aagaacnatc	gtcattcgtg	cgatgactat	660
tcagcccaaa	gagcagcca				- •	679

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 684 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...684
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222

cgccggagga ttcgtatcag ctaatatcca ctcatctgtg tcgggtaagt gctgaagatc 60 gataacgtat acgactcaag cggctatccc aagcccgcgt cttcattagc gtagaaggtg 120 acgaatggga agagggcatc gatcgctacc agccatcgtc aaagaatgca atctggatgc 180 aaaagaaatc gtagccaaat ttctgcagcc cggtattgtg ggtcttggcg gtgctacctt 240 ccctaccatg tgaagetgtc ccctcctccg ggcaacaaag ctgagatcct gatctcaacg 300 ccgtagagtg cgagccttat ctgacgagcg accatgtcct tatctggagc acggcgaaga 360 gatcatgatc ggcgtgagta tcctgatgaa agcattcagg taaacaaggc cgtcatcgga 420 gttgagaata ataagaaaga totattgoto acctoaccaa actggccact gcatatccgg 480 gcatagaggt atgccgttga aggtgcaata tcctcaaggc ggtgagaagc agctgatcgt 540 gcagtgatcc gcaagcaggt aaaaagcggt gccttgccta tcagcacagt gccgtagtac 600 caaacgtggg tacggatttc gccgtgtacg aagcagtcag aagaacaagc ctctggtcga 660 gcgcatcgtg acggtacagg aaaa 684

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...666
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

60 cggatcatac tggatgatat acgtagtatg aacaatgtcg ggtcagtctt agaacggccg 120 atgetttteg gttagaaggg ctatgettgt geggaateea geteggeeae eteateeega catacacaag acagctttag gagccgagac agtgtgaaat gggagtattt ctcttcggta 180 gtggatgcaa tagaagattg aaagcaaaag gatatagtat ctgtgcgata gaacaggcgg 240 300 aaggageeta teettggaaa attteteece eteaaaagge acaegetaeg eeetatettt 360 ggcaatgaag taaaaggagt acgacaggaa gccatcgacc tcttgacctc tgcttagaga 420 taccccagtt cggcacgaag cattcgctca attaagtgtc acagcgggaa tcgtcatctg 480 gcaactggtc aagccgctac tcccctcctg aaaaaataat acccccgaaa aagggggaaa 540 aagagetgte aaggaataag ageeaaatee ttgagagaaa ggaacetett tgeaactaae 600 ttttaggact tggttagtct cagacggcag caatgagcaa ggccacggat aggcggaaat 660 gccttcctct cgtcctgtga agccaagttt cttccgtgtt ggggcttcag tgaaatatcc 666

(2) INFORMATION FOR SEQ ID NO:224

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1812 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1812
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

60 cgtggttgat ctgcaaatcc accgattcta cctttctact aagaagaatc ggatttagaa 120 aaagtgtttt tototatoga toatgcaaaa gggacaatgt taataagaaa tatatgcott 180 atggcacggt tttagattct gtcctaagaa tctcgttacg gatctctctg caaaaaagtt 240 gcaagtagcg gttaatatgg ggagtataaa gattggcata ataaagattc gttgtggttg 300 cgcgatgtca taccttgcat ttaatggttt tcgacgaaag tggcgagaaa acgaaaagta 360 tactgttacc ctcaatcgtt atgattatca accgactacg ttttttggca tatgctcgat 420 ggagtagett taceggatat caatgettet ttgtegatgt tgtaacacat getgaeaggg 480 tttatttggt agcagccaca gtaataagac gctgttgtat tcatctgaca ggaaaaatcc 540 tgttcattgg ctttactatc gtcttccggc ttgtccggtg catgtaggca gatagccgca 600 ctgaagatgg acgcgcttgg attctaacag attccggtat ttatcaaacg atgacttcac 660 aaactggagt ttgctcccct ctgaagtccc tgtgaccccc tgctgggtgc catggtttgg ccacagggaa gtcatacact ggcattcttg ctgaaaaaga tggctctctg ttctttgcca 720 780 ccaatatcga tggagccatt cttggcagga gcaagctccc gaaactttcc ctgttcgcaa 840 tttcgtactc aactatataa agcaaacaat catccaatgc tccgtttagt cggggtgtaa 900 cgcgtacggg tgctcctgcc acttccgttt ggatcacgag catggaaacg attggtttgg 960 acttgacttg gctgccggag ccattcccgc acaatggaaa aaggggcttt ggtgcaaact 1020 ccatcggatg gtaacttgta tattatgcca cagaacaagc cgaaggtata aagcgagtag 1080 ctgtggcatt tcgactgata agggcatcac atggaaacgt ggagccgccg atattatgtg ccggccgatc ctttctacac agccggctat ccgttgtcgt tcgtctggct tttgatgatg 1140

gggcttacaa	tatatatcag	ttgggaggcg	ttagctttca	ggaacattct	tttcctcaat	1200
			aattagtaag			1260
tgccgccatt	gcttgtttgc	agtgtgtaac	ggccggatag	ctgctcagga	ttttctctat	,1320
gaataggagg	aggttttggt	gctgctcagt	attttggcga	tgcaaacaga	ggttgttcgg	1380
ttcatccgga	gtaggtttgg	agttggtcgg	acgttacaat	ttaattttcg	ctgggctttc	1440
agtaccatgt	tggattggcg	tacattgaga	gcgataccga	taagtccggg	aatgtcttcc	1500
ccgattttgc	tcaagcggat	ttaaggtcgg	cttgactcag	ctccacgtta	gaagcgaatt	1560
taactttccc	cttatagcga	tggctataag	tatcttggta	cagctcggct	gtctcctatg	1620
tagcggccgg	gttgtctttg	ggttttgctt	cgggtgctaa	aggttcgctt	ttgctcccgg	1680
gattactgcg	ggaatgggag	tgaagtataa	gcttaaccgc	ggatcaatgt	cggtatcgag	1740
tattctttca	cgggggttac	ttacgatgct	ttggatgcgc	tgacggataa	aagtgtttgg	1800
ctcgaggatc	ca					1812

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225

cgggcagatc	gttgcgcgtg	ctcacaacag	agtggaaagg	ctaaacgacc	tacggctcat	60
geegagatge	ttgccatcac	gatggccgta	gatgccatgg	ggggaaatac	ctccgcgact	120
gcacgctgta	cgtgactgtc	gaaccctcct	gatgtgtgct	ggcgcacttc	gctggacaca	180
aataccgcga	gtagtgacgg	agcatccgaa	cccaaagtgg	gctacaggct	gttcaccgat	240
			gcggtatatt			300
			gccgagcaac			360
			ctcggatctg			420
			acaaactcta			480
			ccatttcgga			540
			tctgcccgga			600
ctggggcgta	ccggcaccct	gcatgtacat	gggccggggg	aatagagcgt	ttcctcagcc	660
ccatattgga	gcagttctgt	caccgatgcc	ctatcaggtg	gagatacata	cgatcgatgc	720
ctcccgacat	gcgctgtaca	tgaggacaaa	tccgtcaaag	tctatagcat	accgctcagc	780
cacccatccc	tgcggtgggc	tacctcttcg	aagagaaatg	ccgtgcaagg	cattgaacaa	840
			tgccgaatat			900
gattacacga	caccggatgg	gcggatcatc	ccaaccgaca	cctcacgacc	ccgggtacac	960
cacccagacg	atatgcttac	gctcggacac	ggagttttgt	ccctccatcg	tccctattat	1020
tcaaggtgtg	atttgctcta	ccatgaagct	acttttatgg	aggaggatcg	ggcaagagca	1080
aagagacttt	ccacagtaca	gccaaagaag	ccgccgaaat	agcacgaagg	caggagcaaa	1140
acgcctcctc	atcgggcatt	actccggcag	atacaagacg	tccaaggttt	gctggaagaa	1200
gctcaaagcg	tattca					1216

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 793 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...793
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

ggttaccggc tetetgaaag tattgcagac ettttaagat cagtaaggtg gtacgatege 60 cggttgtatg gtcaaaggaa ggtaaggtca agcgaacagc aaggttcgtc tcatacgcga 120 cggtatagtg atccacaccg gagagctggc tctctgaaac gattcaagga cgatgccaag 180 gaagtggtgg eeggaeegaa tgeggtetta atetggetea etegaaegae ateeaagatg 240 gtgattaatc gaagctttcg acgagatcga aatcaaaaag actctctaaa gatcaaccga 300 gacgggttac cacccatgaa cgcgatcgat ttagccatac tgaaattttg gcgataggat 360 tactgaaagg cetgtttgat ggtatcatca aaaggcagtt teacttatag ceatagtegt 420 480 tgccacgtat ggttgtgcct tcttgccgtt cccatagaga cgtggatcgg acctttttc ggcctttcac aggcgtggct catacttttg ctttgatcgt tgggttcttg gctattttgt 540 tatcatcccg atggtcggca ataaggtctc gaaaatcgtt ggcaagaccc tatcggcatt 600 660 ctcaatcact tggccggcgg aatagtcggg atagggttag cagctattct gatgagctat cttttcctga ttgccgacaa tgtttttcaa gagacgaagc ggacagtgac aatccgtccc 720 ttcgcaatac ttcgagctgt atgaccatgt aaaaacatag tcccaacttt tagcccccat 780 793 cggcgtttat gaa

- (2) INFORMATION FOR SEQ ID NO:227
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1485
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227

tttccaaca	a coastoctat	+ + + + + + + + + + + + + + + + + + +				
acctaatta	t ttttt	- cogociting	ggtttttgcc	ctgcttgttc	agtctatttt	180
355005	c ccccaccc	, yyaaytqqat	. gaaaaaaccc	r aagattttcc	r cacattaaat	240
	- ccccycatat	. aqueacegaa	i tacateceto	, taacettaa	~~~++	. 300
	- ageageete	. aacaattttc	: actacttcat	tetaatstas	+-++-+	360
	- egeacageet	CCayacgagt	atootaccc	tacttetocc	+++	420
J	, obogeteet	LLYCCCGAGC	agtcatcgtt	cttaaaaats	++~~~~+	
cttattatac	ctgttcatcg	ttgtccttta	tagcatatea	ataaaaataa	gagacaaggg	480
atgcctgctc	cattgcttca	Caatataggg	ttatacacat	stacesta	attttttcat	540
ggttcgtgct	gategeatta	agaatagtoo	tttata	accedatate	attttttcat	600
gatcaatgga	actattagas	ttaattast	cccatgacge	tatgagetga	gcaccatgat	660
aagttttag	, goodcogood	ctagttcata	gccggtttgt	tcataccgct	ttacctgtcc	720
	acaggaactt	coggillata	tcaagccgct	gatcadatta	taaggagagg	780
	egcaagaagg	yaaaqttaag	gttcgaactt	acdaadaa	222+-+	840
gaacgga	cccaacyaca	Lagticcaac	CGAATCAGGG	aacataaaaa		900
	- uccegeaga	guccygcact	gagttgtcag	Catatttatt		960
	gueegeaaga	Cyquategec	ggtgcaaacc	aattaaaaa	2224-4	
cgttgcatcg	gacgaagttg	tagacctctc	agestentina	Caaattagaa	to a ment of the	1020
ccttataagc	tgtacctggg	gtgatgatga	aacacatatt	cadactecad	regggtgett	1080
gtagaaacac	gtactatete	Caacaacaa	attactus	caygaatgca	teteeggeeg	1140
togagoatat	gtactatete	cttatageat	accgacgaat	ccagttcgta	gaacgaacca	1200
actacttttc	ccatcccttt		ccaacgtaat	ctgcttgtcc	agatcgattc	1260
3300000	cagicate	gaacyctttg	gcagatagca	atatactott	~~~~	1320
J- J- Gadaaa	acaccagege	yelytegtaa	tccatacaaa	tagtgccgta	ataaaaa	1380
7	addeegette	acquacacta	TCCCtcaatt	nggatcatat	atattagcaa	1440
agtgaccatc	ggccacataa	agttcgacca	cagateette	aactt		1485
		-				1400

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1337
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228

atccccgcaa	gctcgaaaca	cccgaagccg	taacggcttt	cgagggactt	ccatacctga	60
5555000	gaacegegee	Lougggtagg	Cdaaddcaac	andaadtaaa	0att	
agatatacgg	acgaggettt	ctagcagtat	tccettttt	tttaataa	ggcaagcatt	120
ataccgagge	ggatgccgat	Canada	t	tttegtegee	ggcaagcatt	180
CCCCCtctta		cyaacatege	cgtggcagtc	attaccgaca	ggttggcgcg	240
, ,	gececciag	cyaggeegte	qqccqqcaaq	ctctgatcaa	tagagaaaat	300
) 0 9	- ggug cgg cg	egecatgtga	ccccttcta	caatteactt	20000000+	
gtggatgcct	gtgttcaggc	tgtacgaaga	engentnaag	20220000	ctccagattc	360
aatqtaatct	atctaaccaa	800000000	addycyddyd	acaacctatt.	ctccagattc	420
ccttgactga	Post soct	agecegaagg	acttegatge	catcaaggaa	gaagtcgggg	480
	augigeaata	gracadda	gaagttcaat	atcagtttta	CCCCCCCC	540
J J	ccucyacyac	gcaccqcaaa	tttcaccata	accataccas	aat at amamt	600
atcgccgtcg	cttcattctc	ctcctggcag	tatttettae	atcccggcca	teres to the	· -
ctgggtatga	cccttagccg	tatacacaca	atttant	accedgeea	tcaaatcttt	660
teggageegt	Coastagets	targegegee	guuggeega	attgggcgta	cgacgctctt	720
22.250	oogacegata	rayteegtea	agtgctggca	gagaatatgo	tastasatat	780
yacayagggg	ctttcggatt	gcttttgagt	tatctggtca	tggccctctt	tectegtage	840

					tattcaatcc	900
tcctcagcgt	ggggagccgg	ggaatgatgc	agggegaeat	cacggageca	egeecaacee	
cgtcattttc	ctgatagete	teatetteta	ttgctgatca	atctgctcag	tgcctttatc	960
Cyccacccc	Cigatagete		tarantarat	ataggectaa	cctcatcata	.1020
cctgcctggc	gcatatccaa	acacccatcg	tagaateeet	CCCCCacca		1000
cagatattac	atoctacato	atattatcaa	gatcatccgc	qccgaacgtc	gtgccaactc	1080
cagacaccac	t dege out and		ggggtggttt	anttentaca	gactatgccg	1140
tggatatggc	tggagatgct	egtegtatgt	ggeetgettt	ggcccgcacg	, ,	1200
tgacagetet	acatacttaa	acacgcccat	tgaactcgat	atagaacacg	tgtaccgcat	1200
cgacagosos	9-9-9 33		agaaaataga	aagagaggtc	tacagatcag	1260
cacgctggca	accgtacaaa	aagacaggac	yyaaaacyyu	aagagaggoo		1320
ggaaaaacca	tgatcaaacc	ctcgatctga	tegetgeata	tccggagtgg	aagegetigi	1320
- -		, ,	-			1337
ctcacagtgg	ggcggca					

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...530
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229

cctgaaagta	atateeggat	caaggggtgt	qcagaggagc	atgtcatcct	gtcgcacaag	60
ccatcgaaca	tatctaccaq	atcaccgaaa	cgatcgcttt	gaggcatacg	gcaagggcgt	120
tgatggtgaa	qtcqcqacqa	cgcaaatatc	ttccagcgta	ccatcttcga	ctateggett	180
acqactatcq	tgtcggaact	ttccttacgg	gcacccacaa	attctatctc	cagatcacca	240
tacttactta	agcggtaccg	aaattggcga	aaacggatag	gtgagccttc	cgtccagctt	300
cttaactaca	gctttcgcca	ggtcgatacc	gcgccctacg	gctctatatc	gatatettig	360 420
gaaggacgat	tcaaqaatat	atctcgcaca	taccacccac	gacataaggt	ttecagteee	480
aactgatctg	ccactttctg	cataagacgg	aatatcggga	tgtcgattta	ctaagaatta	530
actctttgtc	ggcattctaa	aaaatcaagg	aatggattgg	ccgacaaggt		330

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1067 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230

gttgtcgatt tgtcttcttt agaatctttg tagaggacgt tttttcgcat tgcagttttt 60 tcagtacacg tcgcttttct caaccgttga agaaaatctc gtcttggacg agggcgacgc 120 cgtagatggc tgagaggcga tetegcagat ggeggcateg ttgeegegaa ggetgaeggt 180 aageetgeaa ttetegeaaa ateetgegag eggatggagg eteeggeate ttteaceagt 240 cgcatacttc tcccagcaaa ggatattcga aggcgatagt cagttcttca tacagatctc 300 ttccttccgg tcggctgctt cgagggcttc gcgagccgct tcggataagc aacgataaga 360 420 cegetegtge ceagettgae accteegaag taegeactae tgegaegaat acctgegtaa 480 qccccaatga ggtgatctgc cgaggatggg tttgccggca gtccccgatg gctctccgtc 540 gtcattggat gtgtgcgttc gcctttggct cccagcttgt atgcccagca tacatggcgg 600 catcgaagta geggegaege agateggeea caagegaeag ggeeteettt eegaetttae 660 aggataggeg aaagccagga ageggetgeg ttteteetgt aetgtgette egagggagea 720 ctgatcgtga ggtaggaatc ttcggcatgg ttcaaaggag agcctcatct gtaccttcct 780 cccgggcggc aaactttcgg acaggacgga gaggagcgta ctcatttgtt tgatactggc 840 gagetetett egeteaette etttttetge aagegeaggg teageagace gtaatggeag 900 traggraagt ctctatctct coogtattgc tecetgract ctggctctaa gctgtacgat ggcagggagc acctgatagt agagteettg aaaateatet etttggggte egecateagt 960 ccgtgagtgt atctcttcca ttgcatgatg gctatgcgga cgatattgat atgcccctgc 1020 togogaacgo ottoggtoaa goatcatott caccagotto ggoatac 1067

(2) INFORMATION FOR SEQ ID NO:231

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...389
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231

tctccggaga	catggccaag	ttgggctata	cgtgaccgta	60
				120
				180
				240
				300
aatacctgac	gcgcgtcaat	ctgtgcatgc	gagccaagcc	360
	•			389
	cggaggagtg gagatcatct gatcgcatac ggtctgccca	cggaggagtg ctcaagtagg gagatcatct tctcgaagag gatcgcatac gatgacctgc ggtctgccca atttcatgaa aatacctgac gcgcgtcaat	cggaggagtg ctcaagtagg aatteeggaa gagateatet tetegaagag atgggegtae gategeatae gatgaeetge atgaageagg ggtetgeeea attteatgaa tateeegggt aataeetgae gegegteaat etgtgeatge	teteeggaga catggecaag ttgggetata egtgaeegta eggaggagtg eteaagtagg aatteeggaa tttegtette gagateatet tetegaagag atgggegtae getttgagae gategeatae gatgaeetge atgaageagg atttegeggt ggtetgeeea attteatgaa tateeegggt gaaacettgt aataeetgae gegegteaat etgtgeatge gageeaagee eaagggeaa

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...457
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

- (2) INFORMATION FOR SEQ ID NO:233
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...495
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233

catategtag geegetaegg cattegeegg accgaateaa caatacetae	ccggcaagac tgtggaagtc aatacgagct ggcagtctgc tgcacgccct ccaagtacct catcaaggag	getetaegge acceteggga egtetatetg gacategete atatetgeeg gaaeggacat	tgcaccttgc tacccgccat gagactccgg ataagcacga tccgctggag gggacgtcat	gtatgcgtga cttcctcacc ccggaagagg ccaaccccaa aggcgtacgc ctggtgccga cgccggattc gacctnacgg	tggaggccgc tatgtacctg gtcaggtgga catcgtggta	60 120 180 240 300 360 420 480 495
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(2) INFORMATION FOR SEQ ID NO:234 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...4\overline{52}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234

cttgaaatta aagatacaga tgttcttgct ttcgtacacc atccaatgtc aatgcggaaa accattctat tatcaatgcc gggcaagaaa gccttgataa gcagagccta cagctacaga 60 acaaattgtt gctacccct ctgtcaagca tatgttcaga atggcaaaat tgttgtagag 120 gaagagtatt ccaagaggaa gtattcaatg caactggtca acttgtcaaa aatgaatccc 180 ttgtcccggt gtctatgttg tccgtataac ggcaaacggt gtaatgtatt tcctaaagtc 240 ttggttcctt gatttataga gctaagattt aaacgaaaac tgcccttctt aatgttttat 300 aagaaggege agttttegtt teteteatte cateteeggg tggtegtega angggaetge 360 ctgtcatctt tcaaacgagg gatatcagct tc 420 452

- (2) INFORMATION FOR SEQ ID NO:235
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1206
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235

	aaaaacttac	atttgagatt	ggatctgctc	ttgaatttct	360
ggttattcat	addageeege	acceptaget	ttatectata	actaaaaata	420
gaccaaccaa	ageeggeaea	aacaccacat	costcocaac	atmamaccat	. 480
caaggacgat	aggggaatat	CCTCatCtat	Caaccccaag		540
actattetti	ctactcactt	qttcccggtg	Lgccccgac	caccoccagos	600
ttagggatta	gtcccctttc	ccgcacctcg	agggcaatgc	eecegaggeg	7 7 7
accctattt	tacaccttaa	aqcacaaaag	ccccggcata	cgcttgagat	660
acgeocaso	atattcaaat	atatatata	gctaaccctc	ggtagcgaca	720
ageceaagg	+====t==t=	acquagatac	attetateaa	gcagcgcgtc	780
cagaacatcg	Legaalacta	tttaataa	gaattaacct	caaaaacctt	840
ccgattgagt	tgtttctgac	tttcactgag	ggettgacet	gagggaaa	900
cgaacagacg	ttgtaagcag	attcctcacg	aattggttee	ggaarreggee	960
tegagttttc	tgagattcac	ggcgagaatt	ttteegttgt	ggcgcgcaaa	
cccacaccaa	acqaaaaaat	tecegageea	cgtttttcca	aacyctaaac	1020
agetttggag	adcasttage	gtatattttg	gtttggtaat	tcattggaat	1080
accertigeac	+ + - +	aacaccataa	tatecteato	gcataccaat	1140
tttgnatatt	Lgagialiaa	aacaycacaa	aggetatoge	aaadccaaac	1200
gatggctgta	cattgcagac	genticitaa	ayyytatege	aaageedaaa	1206
	gaccaaccaa caaggacgat getgttettt ttggggatta acgectattt agetteaagg cagaacateg eegattgagt egaacagaeg tegagtttte eeegegecaa acetttgeae	gaccaaccaa agccggcaca caaggacgat aggggaatat getgttettt etgetegett ttggggatta gteecettte agctteaagg atattegggt cagaacateg tegagttee tgagattee ecegegecaa acgaaaaat acetttgeac ggegattgge	gaccaaccaa agccggcaca aacactacat caaggacgat aggggaatat cetcatctat getgttettt etgetegett gtteeeggtg ttggggatta gteeecttte eegeaceteg ageetattt tgegeettga ageacaaaag agetteaagg atattegggt atgtgtettg eagaacateg tegaataeta eegaatggtae eegattgagt tgttetgae ttteaetgag egaacagaeg ttgtaageag atteeteaeg tegagttet tgagatteae ggegagaatt eeegegeeaa aegaaaaaat teeegageea acetttgeae ggegattgge gtatatttg	gaccaaccaa agccggcaca aacactacat ttgtcctgta caaggacgat aggggaatat cetcatctat caatcccaag getgttett ctgetegett gtteceggtg tgtttttgac ttgggggatta gtcccettte cegcaceteg agggcaatge acgeetattt tgegeettga agcacaaaag ceeeggcata aggetteaagg atattegggt atgtgtettg getaaccete cagaacateg tegaatacta cegaaggtac gttetateaa cegattgagt tgttetgac tttcaetgag ggettgacet cgaacagacg ttgtaagcag attecteaeg agttete tgagatteae ggegagaatt ttteegttgt ceegggecaa acgaaaaaat teeegageca cgttttteea acetttgeae ggegattgge gtatattttg gtttggtaat	ggttattcat aaaagcttgc atttgagatt ggatctgctc ttgaatttct gaccaaccaa agccggcaca aacactacat ttgtcctgta actaaaaata caaaggacgat aggggaatat cctcatctat caatcccaag atgagaccat ttgggggatta gtcccctttc ccgcacctcg agggcaatgc cctcgaggtg acgcctattt tgcgccttga agcacaaaag ccccggcata cgcttgagat agcttcaagg atattcgggt atgttcttg gctaaccctc ggtagcgaca cagaacatcg tcgaatacta ccgaaggtac gttctatcaa gcagcggtc ccgattgagt tgtttctgac tttcactgag ggcttgacct cgagggcctt cgaacagacg ttgtaagcag attcctcacg aattggtcc ggaattggc tcgaggtttc tgagattcac ggcgagaatt tttccgttgt ggcagcttcaccggccaa acgaaaaaat tcccgagcca cgttttcca aacgctaaac acctttgcac ggcgattggc gtatattttg gtttggtaat tcattggaat tttgnatatt tgagtattaa aacagcataa tatcctcatg gcataccaa gatggctgta cattgcagac gcnttcttaa agggtatcgc aaagccaaac

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 626 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{2}6$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

•					aaaaaataaa	60
cogoccatga	gctcggctat	ctcctccggt	ctcgtcagcc	ccttcatcgc	ggacgacaga	
	tanastaaaa	totatoccoa	gcccgatcca	caggaggcta	tgcgtgccac	120
agaggagtgc	Leegalggee	cccacccca		~n+a~nnn	teceaactee	180
ttccatqttg	cgcaaaagtc	cgtgcatccg	tttttgtcgc	yattyaaaca	t t t t	240
atasacaac	tragraacto	catactttct	tcacgagetg	ccgatcggga	geragiguae	
graaaacggc	tougouas og		actocactos	teggeggaga	aaaggtattg	300
gaatcaactc	gegtatgagg	ayayyaaycy	accordeca		gatgatactt	360
tegtatatta	tcatgaggga	tacaggatgg	gataatgaat	agigacgacg	gaccacaccc	
	aggetatogg	ttagaggaga	gggagaaaag	gcgaacaaag	gattcgctga	420
gtagteggaa	agcacacogg		+++ ~ ~ ~ + ~ ~ ~	aggattege	tetgeaacaa	480
atttttttat	ceggettete	ttcgccagcg	cicyayaccy	ageggeeege	tetgeaacaa	540
atectedaag	agatagette	caatcqqtqq	acagtaggct	cgtcatagat	gataccatta	
gecoogaag		atacaasaat	ccatattcqt	agagecgaeg	aagccacctg	600
			Coacacag	-5-5-5		626
actatcacca	ttatcagctt	ggaatg				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 987 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...9\overline{8}7$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

atttcgatgg ctgaatatgc tcgcatatca ttccatccat caaatatgcc tggaagccgg catgatecea caggtacget ttggtateae gtteteteeg tacacaeggt ggagtactae 60 tocattotgg cogatgaget gategeacag gggcaccgag atetgeetga aagatatgge 120 cggtatcggt cgtcctattt cctcgggtca gctggtgaaa tccatcaaga ccaagcaccc 180 egatgaatca tegaatatca eggeeactca ggteeegget tetetgtege tteetgetgg 240 aggtttgcga gaatggggct gacatcatcg acgtagctat ggacctatct cttggggtaa 300 ggtgcatccg gatgtgatca ccatccagca gagctcaagg atgccggctt caaagtgccg 360 gagatcaata tggatgccta ctgaaagctc gaagcctgac acaggagttt atagacgact 420 tettgggeta tteatggate egtegaacaa agagaegage tegetgeteg tgggatgegt 480 ctccccggcg gtatgatggg atccatgatg gccgacctga aaggggtaat gcaggtatca 540 atatgttcct caaaggaaag ggcgagccgg agatgacatc gatcagctac tggtacgtct 600 cttccaagag gtagagtatg tatggcgcgc cttggctatc ctcctttggt aactcctttc 660 agccagtatg tgaagatgtt gccctgatga acgtgtacaa catgatacgg ggcgaagggc 720 gttgcaagcc atcgaccaga acacatgggg tatgatecte ggcaaategg geetttgeee 780 ggcaaacteg ateeggagat categetttg gcaaaagaga aggaatggaa tttteggatg 840 ccgatcctca gcaattttat cctgatgcct tgacgaattt cgcaaggaaa tggatcagaa 900 cggttgggag tatggccaga gacgaag 960 987

- (2) INFORMATION FOR SEQ ID NO:238
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 583 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...583
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

aacatggaca agaaacacga	acgtagccga tgaggctcgg	caagcgaatg	tgagcgatgc	cgacgacaat	atgtaggtet attetattte atcateggta ggtetaeegg aagaggtgtg	60 120 180 240 300
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		caccetetat	attttgagat	tctctgaaag	ccggatttaa	360
tcaaaatgaa	aattttggct	+-+++	catttcctct	cactttttqt	cgaagctgtt	420
ttataaagag	gctgtgttga	aattatttt	-t-resttta	etttaacaat	togggagatt	. 480
tggaatttgt	cgaggcctct	gatgggggtt	gregearry	acceggegge	tegggagatt	540
ctttctcata	gcatcgaaat	agcagggtgt	agaagtcggc	ttttggtcct	atttttgtgc	583
tatgttgggt	gtgccgtaaa	aacttgaaaa	agcgaggtac	ggt		505

- (2) INFORMATION FOR SEQ ID NO:239
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 785 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...785
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

ccggaaatag gagaatggtt gcttgcaaac gagtcggccg tatctgccac gaagtggtaa 60 agggetttet caatetgace attgeteega gggtatggtg gagetgetga aegagateeg 120 ageggatate aactteggae ataaggtget acagaggata geeegetggt aatggtggag 180 tattettete egaatacaat aageegttae acettggaca egtaegtaae aacetattgg 240 gttatgtctt tccgagatca tgaaagccaa tggctatcgt gtggtgaaga ctaaatcgta 300 aatgaccgag gcattcatat ctgtaagtcc atgctcgctt ggcaaagtgg ggagatggtg 360 tgacgccgga gaaggccggt aagaaaggcg atatctgatc ggagacttct atgtcctttt 420 cgataagcac tacaaagccg actcaattcc cttatggctg aaggtaagag caaagaagaa 480 geogaageeg aageaceete atggetgaag etegtgagat getaegattg tgggaggeag 540 agacgaaaag gtcgtcgatc tctggcgtac tatgaatcag tgggtataga cggattcgat 600 gccacataca agatgatggg tgtagacttc gacaagaata ctatgaatcc gagacctatc 660 tegteggeaa ggaagaagtg etgagggttt ggaggaagge tttgtttgte aageatteeg 720 780 atggtttctg tatggcggat cttgacaaag gatggcttgg atgaaaaatg cttttgcgtg 785 ccgag

- (2) INFORMATION FOR SEQ ID NO:240
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 631 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION $1...6\overline{31}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240

cccattcaag ggcagattgg attactttat tagtaataat ggatatggcc tcgtagaaag 60 gcttatttcg tatatatcac aaaacttatc ttctatattg atatatctga aacgctcatt 120 tgtttgacat agagtgagat tacatgcttt caatataaag tttccaactg ttcatcttcg 180 ccatgtacag gatgcttcct cctcggatta ctacgggagc tccgttgcca tatcgggttt 240 tcagagetat accteatage etttaggete etegaettag geaateecea tttaettgea 300 taatctatta gtgcgacaaa ctgtcggatg cgacgttcga cctttgttca atccgtcaga 360 ctacaccgga aagtactacg gagtggcgtt tgaattgcct cccgtcacgg ctcatttaac 420 ageototgga ctatogttoa acaattoagg cttoateott gtgottgtot ttotacotog 480 teatteagte ceaettggea attagtggae ttatgeettt aetgaeatge tacaeteeet 540 600 tgggtttccc ctttggataa gtggttgata gtaggttact tcaaagaaac gaacctaatc 631 tatagctaag gagatattta ttgtgctgcc t

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 995 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...995
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241

4	ccggagcatc	ttgaagcgtt	tcgtagcatg	gagtgcatgg	ctgacgttgc	cggcatgatg	60
				tggcctccat			120
(ccaatatctg	tacgaaggca	tcgaaagtgc	tgtgtgttcg	ctcaatccct	gcccttggtc	180
				ttcttaagta			240
4	ccgtcgaata	ctctactgat	gccgatatgt	cgaggacagt	agctttgggg	tatgttcttt	300
1	tgtcattgtt	tgttttcgat	tgtttagtct	gatctcatgt	ctttaaacgg	gcatggcatt	360
1	accettattg	cgtcggagag	agcctatacg	agagagggtg	tgccaaacga	aaatacttcg	420
				gcctgtatct			480
				catattcgcg			540
1	tatctgtttg	tacatgacta	categteete	caccttggga	gctaccttcg	cagetegeeg	600
ě	agcatcttct	ccaagaacgg	agacgtcttg	gtcggacgcg	gaattcgaag	gettgggeeg	660
•	catcgaggag	ttcgatggcg	aagatctctc	caggttttct	atgatcggaa	gcagctttcg	720
1	ttgctgcgtt	agctccatag	aaaccgtggt	cttcctgccc	gttgctgctg	acgatactat	780
(egetgetgeg	gagaaacagt	acattcttgt	tcttgctcac	catagetgeg	gctcatactg	840
9	geggtateat	gaatcccgct	gttcagaccg	gggattggct	acaggaactc	aggcagattg	900
		-		cttcgctgat			960
			tgcaagaagt				995

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1081 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1081
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

aatcggtcaa gtgtgtggct gccaccgtga agaagccgaa gctctgcgat caagtatcta 60 agcaaaaggg cgaaatagcc gtctgttcga tgacttcgct ggtaccgtcc gaagagaaaa 120 agcaaatcgg acaaatgctc aatgagcgaa aaacaaggct caggagcata tcaactccct 180 tegegagegg geacageagg etetgeacaa getteggeag aaacegaeet gacaegaaca 240 tcataccgac gagactegga acaegecate egateteeet ggtgaageag gagactgega 300 gatetttgee egectegget teagtatege egaegggeeg gagtagagga egaetggeat 360 gtattetett egatgaattt egeegaagae eacetgeteg tgatatgeag gacacattet 420 480 teategagea tegeceegat geatectteg caegeatacg tecagtgtee aaageegggt 540 gatggaaaag cacaaccgcc gattcgcgtc atttgccccg ggcgtaccta ccgaaacgag ctatetecta tegggegeat tgtttettte ateaggtgga ageaetgttg tggaeaagga 600 tgtttettte geegatttge ggeaggtget tetttaeteg eacaggaaat gtteggagee 660 gaaaccaaaa tacgcetteg eeettetatt teeeetttae egaacegtet geegagatgg 720 acateteetg caataatgtg ggggtaaagg ttgcaactte tgcaagcata egggatgggt 780 840 ggaatactcg gatgcggcat ggtggatccc aacgtattgg acaactgcgg catgacagca agaaatacag cggctatgcg ctcggtatgg gtatcgaacg tacaccaatc ttaagtaccg 900 agtcaaagac cttcgcttct tctcggagaa cacctcaact tcttggaaca gttcaagagc 960 gtgcactaac cctctgatca tatcgaatgc gcaaggaaga gcgatacaaa gccgttatcg 1020 attggtttge gagaatatge eggtggeega aaeggagetg eggtaceggg ateettteag 1080 1081

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 626 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION $1...6\overline{2}6$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

cgtgactttc cctttctctc gtaccgtcat caagagctta tagagatagg atgctccgac gtecatgtat gtaccgtace eggetgtget tegaaagaag ggtacgetet eegeeggeag 60 ctatgagggt cgaacgggtt teggtgggat ggtettteet teggeatega geaattegta 120 tgtcagagat agctcgaggc ttcgccacgg cggttgcgta agtcggcttt cagggagaat 180 atacettgeg gtagetatea tegagtgtgg atttgatget gaaateette actgegeett 240 gggttgtgca aagaggaata catcgcgttc gatcccactg atggccagaa gtcctgacat 300 tocagatacg agooggtact coaacgatag acttgagogt gagogtgttt tttcoggoat 360 ggacataggg attgatgagg attcggccgg attcttggag tcttcgctgt agcccgcttc 420 gtgtccgttg tatagacata gagtccggac ttggctccgg ctatatggag gtagatatcc 480 getecateca gecegtgggt aettetatet egegeegata cacacetagg ggttggettt 540 ccggcagttt gggcggctgc ggattg 600 626

(2) INFORMATION FOR SEQ ID NO:244

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 603 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{03}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244

cagegactge tegaateeet etetegtegt eggagggaeg aagtggageg egtggtggee atgtcgttta cggacttcag ccacgaagcc gtctcttcgc tatcgtgccg ctcccgatga 60 gcagcacccg atgataacct tttgtctttt tcgctctttg atgccgaagg tcgtcaccca 120 tagacggggg aaatatccca agggcaacac agtcgccacc atcataaaga agagccgcag 180 gtagacgccg tgtcgtgtac gatgtcgtcc accacgagca gcagaaagac gacgcggatc 240 cgaccagcac cgacgccacg gtcgtcagca gttcggatat tcgcttttgg ctatgggttt 300 gttgtagtat cccgagaggg cgaagagaga gaccagaaaa gcagatagag gatcccacc 360 cacaggetet tggegttgaa ggatattegg acagagtgga gtatatgege tettgetett 420 ccgtgaggta cgcagcgtat tgtagctcaa ataggaagcc acaattaccc gaagacatcg 480 ccagcagata gegecaggeg gtgtagettg cataegtgte aattggegat caacetecae 540 ttc 600 603

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 776 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...776
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

aagaactttt acggctgccg ggatggcaca gttatatgtc agtcgactag tgagcgtgct 60 teggggttge tegetatgea caaagaeetg eeggtegaee ggtegteagg etgatgageg 120 aaatagattt gcagtteate acgeaectea geeegaeetg teegaaeteg aagaagegga 180 ggccgtctgc cgtatagtgt gcgctgggta cagcttcgga tgaaggangc ttcggacgaa 240 300 natatettea eacggettgt geegtenagg etgtetgeeg teaccaegga geacttttgt cgtcnatgac cgtgtccaaa tnacccgtca ggtggatgct gacgcgtaca cttgggcaaa 360 gaagatatgg cgatagtcga agcgcgtcgc atctcggttc gaataagatc ataggacgca 420 catgcaatac gatggaggat ggcgccgagc atatgccgaa ggagccgact acgtgggtat 480 aggecegtat getataegga gaegaageag egtttagete eegteetegg aetegaaggt 540 acaaagccat cgccgcctgt atgcaagccg aaggcatccg actgccggct ttgccatcgg 600 tgggatagag gatgcagaca ttcccctcat tcgcgacgtg gcataggagg tattgccgtg 660 ageggeagee ttateaggaa aataaaaaga aetaategga tgateteeet teegtatega 720 776 acgatcatct tttgaaaaca ggaaaaaatc taatggaaac gttacaaatt gccggc

- (2) INFORMATION FOR SEQ ID NO:246
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 858 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...858
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:246

cetgatacte ttgctattca gtgccctcgg tgtggtcgca acccgtattc acactttttc 60 ctccgcttgt ccaatgccgt tttgtatggt caggagcggt ctttctggtc cgtatgccac 120 gctatatcag ttatcggctt tttgtcttat cggccgtatc caaagcacat tgttgctctc 180 240 gatctgttgt ttcctctatt ggacgacaag gggcaactca ccgatttcga tttgtgggaa 300 agoctttttt cttggctttg ctcttcttcc tgttctgttt tgtcttttgg ctgtgaggat 360 gttttatgcc ttgtggtgct atttctttgc cgatcgtgag actagatgat ctggagaggg ggttatgcgt tgctcgaatg gatgtggggg atctcctttt tcccgttgcg gtcatctatc 420 tttatatgcc acaattatat tgctaagcta cttgttacca gctattttcg tgctgtggag 480 attagtgctt tcgctaaaac gatacgattc ttctcgatca gggaagtagg tttttccac 540

tttctttgta cctttgtgcc-cacgaaa	attt taccgttggt ttacttgatg ccttattgga 600
gtggtcggta aacaataaag agataat	tggc tctatggagt aaaagtaaag aagatactca 660
tttcacagcc acaacccgta gcgggtg	ggtc gccttattac gatattgctc agaaacatgg 💢 , 720
ctgtgaggtc gtgttcgtcc tttcatc	ccaa gtagaagtcc cgtcagtgcg agagaatttc 780
gcaacaggaa agtgaatatt ctaagac	ccat teggecatea tetteactgg acetaceage 840
tatcgaccat ttttcagt	858

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 659 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...659
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

ctggcagtgg aggaactaag ccgtgtatgt gctaccacag gcgtggttcc tctgcacaca 120 catctttgtg cgcagctccc atctacgaaa atggaacaaa gaacaaaaga tgaagtattt geogaaacte tgttetggeg aatggatggt geatttggae ttaeegaace caatgeaggt 180 240 acggatgctg ctgctcgcaa acttttgctg aagaaaagga agatcatttc gtacttaacg gtaacagatt tttatcacca atgccgaata tgctcacgta tacgtggtat ttgcatgaca 300 gataagagcc agggcacacg tggtatcacc gctttcatcg ttgaaaagga actcccgggt 360 420 tetetategg aaagaaagag ettaagatgg gtteegtggt teggetaeat gegaaettat 480 ttttgaaaac tgtatcgtcc caaagagaat cttctcggtc gcgtaggcgg tggcttcaag ategocatga aaccettgat ggeggaegta teggtatege ateteaggee eteggtatte 540 600 acagggagot atggacgaga cggtgaagta caccaaagag cgtaaacatt cggtcgcagc atogoacaat ttoagaacac goattocaac togtogattg caatgoogat ttoagcato 659

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 662 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION $1...6\overline{62}$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

				~~atattatt	ggttcctgaa	60
cgggggattt	ctttgtggag	tcgccgatca	tcttgctggc	ggotattatt	ggcccgcgct	120
						180
tatgcgcaga	tettteegat	Cotgactet	tesasttasa	ggacagatcg	cttcggccaa	240
						300
						360
						420
cgacaaaata	tetattegge	ggcaccogge	tatogatgag	ttgcccacca	aaactgatca tctacttccg gtctgggctt	480
						540
						600
	+ + o o	addcdattac	uuauacuayy	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	_	660
Caggacccca	+ *+++cacc	antcaaatca	taggtgaacg	gcccagacgt	tatcggaacg	
cggtgggaaa	tgttttcage	ggccaagees				662
ct						

(2) INFORMATION FOR SEQ ID NO:249

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 584 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...584
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 899 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...899
- (xi) SEQUENCE DESCRIPTION: SEO ID NO:250

ggcaagtatt gcggcagcca tcgataccac acgtatcgga gttgcagcta aaactgtgcc 60 gataaggagt cgggtgcata taccggagag gtctctgcgc tatggtagcc agtaccggtg 120 ctcggtatgt gattatagga catagcgacg ccgtgcttac tatcatgaaa catccccaat 180 cctgatggag aaggtgagtt ggctttgtcc aatggcttga cccccatttt ctgtgttggc 240 gaagttttga aaaagcgcga agcaggcaag cacttcgagg tagtcgctcg tcagtggaag 300 aagccctgtt tactttggat cagaccgact ttgccaaatt gatcttgctt acgagcctgt 360 gtgggccatc ggtacgggta agacggctac ggagaccaag ctcaagagat gcatgcacat 420 attcgtaaga gtatagccgc taatatggaa aagaggttgc gaacggttgt tccattctct 480 atggaggcag tgcaatgcag ccaatgccaa agaactcttt agccgtgcgg atgtagatgt 540 gggcttatcg gaggggcttc tctctcggta gacaaattct tgcctatctc gaagcattct 600 gagattgett attgttteae accetttegg gegagtttat tteaaaagga gaaaegaaeg 660 agatgaaacc gattttcttt ttagtcccta ttgctttcgt tggtttgcca ttcgtcatcg 720 gaageteagg ttteecateg geteatagea aageeegat cageatette gaagetetea 780 gtgcgagcac gaaggagaag gcatcatcac catctatcag cctgcatccg taagctgccg 840 tgggcaagta tccggacgtt ggccgnttga tcganggcga gacatatccg ttgatccaa 899

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...395
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251

catcggccat	cacacgagtg	atgagcaaag	gagcggtacc	gctgttgcga	acttgaagct	60
atgccctacc	gatecttttt	cttccggaat	caggccaagt	taaaggactg	ctcctcgacc	120
rgtatttccg	gactctcctg	agctgtcgca	acagaggagt	caataggaaa	aggaagaaga	180
gcagccctcg	aaatgtctga	cgatcatacg	ccttgtacta	cttgcagagc	tatgctattt	240
atteteaace	cctttgatgc	gtagcgtaaa	ggtaccatcc	ttaccattgc	tgtaacggct	300
atggtettta	cgaactgacc	cggacggccg	gcaggattat	atggacgtct	attttgcttg	360
cctgacccgg	agcgatgggc	tctttgctaa	acggg			395

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...618
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252

cttttccca gaagagaatc cgcatttggt cgtatgcctt	gaataccetg tecgacaget ttggetegte aaggaagtet acaccgatga gaatgagate cagagettta geatetgetg	ctcgttggcc tcttcacgag ctgaagccct gccgtaggca tcttgcccgt gaacatctcc gggtcgagcc caattgttct	tgettgatac cttgeegagt ttgteeactt tteettegat agegaaagee teteggaetg accaetetga ttgtteattg	actacgcate tegggaaacg teaggaaggg ettgeegege ggaaagtaat atatgcateg tecaatgete ettgtetatt	getteateag gaegatgtgt atggaegtte catecgagta ggttggatae ctacaaagce ttaataagat	60 120 180 240 300 360 420 480 540 600
gggagcetga agegaaatag eggttegeae	cttgtggttt	ttcttgnttt	cctaaaggta	gagattattg	tgagaggga	600 618

- (2) INFORMATION FOR SEQ ID NO:253
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 578 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...578
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253

tcgagacagt	ctgaatcagt	tgcaatcgac	caaataaacc	catacacaat	ctctttagcc	120
			ctcgaacgcc			180
					caaatagatc	, 240
			caaagacgaa			300
tacgattgga	tccaagaggg	acgaacggag	attccgtccg	caagaggcag	gagcttcgtg	360
			tctcgacaaa			420
			attatcgagg			480
gaactgattc	agctggattc	ggcttctgct	ggaaaatctg	gatgaagaat	tgaataattt	540
	ttcttccgga					578

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1073 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1073
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

60 cccgtgcttg tctcctcctt gctgctatcc aaatagagga tggccgaatg acgaagccga 120 acagactett tegegaetga agaategeee geaatttggg atgaageega tgettatate 180 geggaaatee aactgttgeg aggegacace gegaagegge egaaatagee gacagactet tgtcgcgcaa ttcgccatga gacagcgacc tcaactcctg cgtgtggcag gcaatgctta 240 300 ctacctttgg gcgattcgaa caaaaccatc gactatcttt ccgactacag cgaaaggtgg 360 gggatcgtat cgcgcctgcc gatgcttatg cacttggtgt cactactata agcaaggtct 420 gatgaaagaa gcacttcggc cacttgccgc tgtaccactg acgccggttc tctcggtgca 480 gagteggete tetatetegg aaggeacage tggeegaggg gatgaegage gaggeeetta 540 tggctttcga aaggctgcga ctcaggacgt caatcggccg gtacgggagg tcggaatgtc aatatggcta tgctcatgcg tagtacggga cagtcgagct tcggtcagcc gtacgcattg 600 cggagaactt cetcaatgag ttteccegat etteccacge gaacagatgg etgetattet 660 720 cgtcgaatca tatttcaccg gcaaggttac aattcttccc ttagatcgat ccaaaagatt 780 gcacageega eggeteeatt etggeegeea aacagtttgt getgaacegt atggeagaac 840 aaaagaagca gcgggctatg acagtgaagc actttctttt gtgtcgagca gtaatctatg 900 ggaaacaaag gggaatattt ccctgaagca tatttcctcc gagcaatctg cggtatagag 960 eeggtgactt teegaetgea getgeggatt aagageetat ateteggeeg eeggtgateg 1020 tgatgcggcg aatcttcctt aggatattat cgtctgggct attctctatt caatgccgaa 1073 cgttacgatt ggctttggag gccttccaag antatgtatc ccnatccggt att

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1933 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1933
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255

cggctgaaaa aaagctgacg gcttaccgga gctattctcc accgatacga aacgaatcgc 60 teeggaetea tegateagea ggagttetaa tteggeegtg gtaeegatgg geggeaagtt 120 teccaagate gtteggeaat etttegtgea gtegateget gteeteegea eteggeatag 180 tocatagete acgageaaat teaggetgte tattatggea tggatgtett eegaacaace 240 tgcctacgag ccagttcgtg caggaaatcc cgattcatca ctaccttttt actggcgtat 300 ccagatagec tteggegagt tteactgett tgeegageat gatectaeeg ttaeegaaeg 360 gacagaaggg aaggaagcta cacaactgag tgttcgccga cgaaattgcc atactgcaca 420 aaggeetgtg gaatgagtge egataggete ettttacata aegeteaete ttggeteeeg 480 540 aattgaggac atatgattgg ctcccaaggc ggtggcaata cccacttgct tacggatgga ccaacgaacg cttcggcccg aaaaaggttt cacgactccc gatgttccat aatagagatg 600 ccgtcccgta tgccgagtcg gggattgaat gtctgggagc agcctctcgg ccttcgggta 660 cgctaatcgt aatatccaca cctcccgcgc atagagtcgg cgtacctctg ctgtcatcat 720 780 tegtegaggt acgagttgat ageeggacet eegaceteea gaeegaggee ggggagegte actaccccac cccttcaccc tgcaggaagc ggacttcctc atgttcggga ttggcctgat 840 900 cgtagegeat accgecatge cattggteae atceggatea teectgeate ttteaggaet 960 geggataega cageatette tteetetega atteegetat gggeagaetg actatttege 1020 cegaaggcaa ttetaeggga etteggegag agagecaage eecateaate ggtaeatgge 1080 tgctactacg cagcggtage tgtggtgccg gtagtgaate egetteggag tgaaaagate ccggcacgag gcgttctacc gcccgtctca aaccgacagg cccgcctcgg gaatgaatga 1140 aggaggcaaa ggggggacgt acgacggcat atatacgatg cccatccgtc gggcagcttc 1200 tatettttet eggaagtaac egeteeteeg etttettttg tgataatgge ateggggega 1260 acggettgea teagteeteg teegeatgeg gttegaagaa aacgatgege teegeaggaa 1320 agogttette tetgecaaag caaccgatte gtetegette aatatgegge aaaggtggtg 1380 egetetttee agaaageage cagettgggg ategtattea eeetgtgage ateageagae 1440 1500 getgeacgee ategecaage ateegetegg ageegtateg tagtttgeac accagaegat accttetteg egtggaggga ttgteteteg tatettaeta eggggataee tgtttgttea 1560 gaggettege cactgaageg tgcaattett eggegaaagg atgageegge gteeaegtea 1620 gtcggatctc ttctttccga caaaacgaaa ccatgtcggc aaccgtatgg ctcctgtcag 1680 1740 acgatggccg tggctactct ggatctcttg cagatgcctt ttggtgggag tagaaaaacg gactteeege tteateeage acgeagetge ggeaeggent teeegtagta eegegaagag 1800 taggatcatg tgcaagaagg tgtttgaatt cgtcggcata caaaccgtga caagcccttc 1860 1920 ccaatggcta tggcttctcc acgacttcat cgttgtcagg tcaaggttgg tccttttacg 1933 aattctggcc aat

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 565 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO



(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...565
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

cggcttggta cgttttctct gctttaggct tctatcctgt tacacccgca cggatcagta 60 tgtgctcggt tcgccgattt tttccaaggt aatactcttt ttcccgacgg acacaaaacg 120 gtgttgcatg ctccggccaa cagtgccata cgccttacat ccgctcgatc agcgtagaag 180 gaaaagaatg gagetgaatt acetgaetea egaacagett egetettetg catecattea 240 atggagatgg acacgaaacc caattataat cgtggtatga aggaaagtga cagacttatt 300 360 ccttctccac ggagcaacag cgtcgcgcta atcacagtaa ttatgataca tttccccact toggactatg aatacqaaca aagcatttac gooogacgat ctatactgat gagcttgott 420 ggetttttee teettgtget agetetgeeg gatgtaaaga tgatgteeag accgacatat 480 ttaaggggee gtggactaeg tgaateetta tatgggeaat ateagteate tgeteattee 540 565 acttttccca ctgtgcattg gccca

(2) INFORMATION FOR SEQ ID NO:257

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...652
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257

cgcgcgtagc	acgtgtggac	ggccgctata	tcgtcaatcc	tactttcgac	agctcgaacg	60
			aatggacaca			120
atggacgagg	tacaggaatc	cgaaatgtcg	aaggcatacg	cgtggcacac	gaagccatca	180
aggtacagtg	caaggccagc	tcgaactatc	cgaagctgta	ggaaaacttc	aaaagcgtga	240
atacaccatg	aagtaaacga	tgaagacctg	cgcaagaaag	tgcacgacga	atgcatgctc	300
gtgcctatga	ggtggctacc	agcggaaccg	gcaaacacga	gcgggcgaag	cttttgaaaa	360
gatcgtggaa	gagttcaaag	ctcaatatac	ggagaagaac	ttgccgagaa	ggccgaaatg	420
atageteget	actaccacga	ttggaaaaag	aagcgatgcg	tegtgecate	ctcgacgaag	480
gcaaacgcct	gatgggcgta	agaccacgga	gatecgteeg	atatggatcg	agaccgactc	540
ctacccggcc	cgcatggctc	agctatattc	actcgtggtg	agacgcagcg	cttacgaccg	600
ttacgcttgg	tacgaagagc	gacgaaaagc	tcgtggagat	gtactcatta	tt	652

(2) INFORMATION FOR SEQ ID NO:258

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...738
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

ttgttcgttt gggtgattcc atgccgaacg agacgaaggt caaagtctct ctcgcgaagc 60 catteettee gateeggeae tgateateta tacateggea etteeggtag gageaaggge 120 gtectectee tgeacageaa tetgatgate agatgaaagt eeatagegag eatateeeeg 180 totatgggcc gggcgactgt cgatagcttt cctgccgatg agtcatattt tcgaaaaggc 240 atggaactct tttgcctgac gacgggaacg aggattgcca tcttgagaga tccgagaaag 300 tattggagge actaceteag atacgeecat egeteatgtg caagtgeeac gettttggga 360 gaaagtgtat cagggcgtga atgagaagat ggctcctctc cccgcatcct gaaaggtgtc 420 tacaggogtg ctatggcogt agocaacgot atogtotoga ctattggaat gaggggaago 480 gtgcgccact cttctgagta tgcaatatgc cttttacaac tgcactattt ttaccctgcc 540 aagegegtae tgggaetaea gegagggegt tattteeeea eggneggaea eegetategg 600 atgagatcaa catcttoott cagtoogtaa acattooato attgtoggat atggtotgto 660 720 cgaaacgact gccacggtat ctttcttccg cagcgaggat tcaagatcgg ctncatgggc 738 aaagtgatgc cgggcgga

- (2) INFORMATION FOR SEQ ID NO:259
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1274
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

caaacctttc gattagttta ttgcagagag ctgccgtaaa atatggggca gaggtgtagc 300 aqcaqtaqqc atcgttctga aaattgtaac attgggaacg aactggtttt cggatttgtc 360 aaqqqactcc aaccgatggc tggctataac taggggcaga aaatttccaa aggttaaaag 420 aggraqtacg ttgttccttg aactgacaac ctcattttgt gtactttgga gcactttcat 480 actogttttt cttctcctgt tatcagttgt ttcggcaaag acgaaacaat gcaagaaatg 540 cacgaattgc ccttagagcc aatacgctaa tgtttttcac tttcggctcc agtttgtgta 600 ttccacacta tatatggcaa tcggaagagc aagacaggcc ttttgctcaa tattggacga 660 cagggactct tetttattee tgtaatttge tgeteecate atattgggga ttgaacggag 720 780 tgctttatgc acaacggtag ccgacgtctt tgcaactttg atgacactgt tctttgccat 840 tcaattcata gggaaattcg tcataaatca catctcacaa cagagaatct acatgttgaa cataaaagat atgattatgc taagacttac tcaaactgaa gatttaagac aataatctct 900 ttatgctcta caaaaggaca gatacaaaaa ggtcagacaa ctttattctg aagattattg 960 ccctatgtga tgcagaaaga atttagtctc attgtttcgg accctccgtt atacacgctt 1020 1080 ttgcctgcac ctttgcaaag gggagattca atggacggag aggggaaaaa atgtatcaaa 1140 ctgctctttg tcattgacac ggagettgaa ttactgaaaa tgcgaatcag ggacttcttc 1200 ctgcattgcc agtcagacct gctaagaaac tctgttgaca ggcaaagcaa cagattagtt 1260 gaactccttt atgctctcga cacttcaaca gtatcaacaa ccgagaaaat agtgtagagg 1274 aactggcaga cgct

(2) INFORMATION FOR SEQ ID NO:260

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 857 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...857
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260

cgaagacgga cagggcgtat gaagcatagg cgataaaact tttcgcaaagc ctgcaaacag 60 120 ataaqqcacq cactcgattc gtggtggaat cgggtgcggc ctcttttata taagctcggg 180 aatgggeett ttgageegte egaactaata taaateagat aegatetgta tacaaatgga 240 aaacgatttg tatataaacg aaaacgatct gtatataaat cgtttttgat ctatatacag 300 ategetttge aaagagtttg aaageatggt eegaactgaa aaagtteget tttetgettt tttacttcag gatctccttc ctttcaggtg cttatttgga atgttccaaa ctcgtcttcg 360 420 ttgttgaaaa ctttttcggt ctgtatttta ggctttttgc ccaaaatcat tctctatcgt 480 acceptcecc atagatectt ctegegeget cttcctegeg gatacegaace aagaggatag cgagatagac ggcattccga cacagaaggt aatccaagca ttgcaaagga gggtgatacg 540 600 ataagctccg gaatgacgtt gaggaaatag ttgggatggc gtaccgtctg aacaggaagc togtttogat acgatgatog ggtacgatat agagettage gtecacacat coetcagett 660 atagatgacg aagaagagca tggcatggca aaaaccaaga tcgctacgcc ccagccggat 720 agogtattga actogotoco gtggcatacg cttcgtacag ggaagtgaag taataggcta 780 tgtggccagg gtgaggaaaa gcgaattgag cttgccatac tgtactgcgc cctgcgttac 840 857 agtcgcttct ccgttga

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 605 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...605
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

eceggtgatt atgatgaatt gettgtttet teggtggtat eggaeaggag gagaggaeea 60 ttggattctg ccgatagcga cgacaagatt agaaaaattg ctgacatatt ctattcaaaa 120 gtagtgcccc gatcggtaag gtcgtccaac agctcagtaa cgtcgtccta acagatcggt 180 aaggtegtee taacagttgg taacgtegte ctaacagete agtaacgteg eectaacgge 240 teagtaggte gteetattee gatgtgaggg teatecette tgettatatg ggtttttgtg 300 cttgtaggaa gacatgccgg aggtcgttac cttatcattc gaaaggctcc gtaattttcg 360 agagaggata tgccggagag atctccccgt acgactcgga agcattgatc ttcaccgatg 420 cegtgecact gacggatact tggtacgttg ggtaatgaaa teggatgeat cacaaccaac 480 ageteegetg atgagagegt gaacteeteg eeggageett teagtttgat aeeggaagee 540 ccgaagcgtt tatatccaat gctctgagac ggccggtgag gtttacagag aagcttcccg 600 605 acagg

- (2) INFORMATION FOR SEQ ID NO:262
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1429
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262

teegagggne ateaatgeeg gettteeget tgttteggge tgaagetgtg egageaette teecaataat ettteggeae tatategteg gtatetgtge	ggntcgcccg tgctgccgaa gtgagaaata	gtcagcataa ggttgcagtt gaggatggct	cgtcgggtca gcatcctccg	cacagaaacg acagagcggt	240
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teteteette	gaaggaaaat	tegateceae	. дассададаа	atttqqactt	ccgacagete	2.50
ctccgtcct	, ccgtcttcgg	caaaggetee	Caataacaa	ctacaaat	atgcgtgcta	360
agaatctcgg	r cggagtagag	Caccaacata	ctttcaatea	etgeaagtyg	gatacaaacc	420
aatcgatacc	gtcacttccg	acttacctet	arte	accegiated	gatacaaacc	. 480
gcatcgatgg	tagcgaaacg	ctccagtcat	- ggrgagegrg	cctgtcttat	ccaagaccag	540
ccgagcgtcc	gatecetaca	aggage	teggeattge	gtacgaggta	ccatttcgtg	600
	y a cococacy	uccayaycca	Laggegtace	902000a+-		660
	you oo ya ca	- cyycac dadd	agrecerada	CCCCSSCCS+c		720
	uauauag	graayyatgg	atagecegat	Cactatacat		780
	agooagac	4 L L Y Y A L A G G	COCTTTOCTO	acctatacat		840
	Jeeegageac	- Grandaria	CCTacataaa	taactataaa		
	J-1 J ~ 5 ~ 6 ~ 6 ~ 6	guguaaacca	LUBUCCUBCE	ナクナナナクナクナー		900
		- cycacyyag	CEGCEGCCEE	COOTCOOCS		960
ggtatetgee	gcccggacgt	acqcqaacqa	agtegetge	asaasaasa	accgtccacg	1020
cacggntctc	gcatccatta	Cacacasca	ageogeeege	gacgagegea	gcaatgggat	1080
cacqaatqqc	gegteegttg	Cttoggacce	aatgeeteeg	ccggctgagt	cgcatcagtt	1140
aaatgcgatg	ttgccccgtg	acceggeegg	cacgetttee	atgagtttgc	ccagtaggac	1200
J - J J	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	aaycacdaag	Lagaggtgga	acttostace		1260
		u coaquotat	annaaaaaaa	matamtamta		1320
J	gaaaaca	Cuculadea	Cadtractta	24+4444	ggggaaagtc	1380
urrectgece	atgtgtatcc	gggcaaggct	atgagcatca	taggtaggg	3 3 3 3	1429
				22 223		1443

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{4}28$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263

gaatcagtte ettetteget atc cegaetetet tetettatga tac teatgeeceg tatggatteg tte tgagatgttt egegggaaga aga geeaagaagg aaaageaege etg tgaatatgee atgaaatgeg gea	cgctggat ggcatctage gccgagca tttccgcact aaggagac gttggacaaa gccaatct ccgacgaaga	tttttgtcgg tgtccctgtc tcgtctggcc	gagaaacgtg aaaagctgac ggacactgaa	1140 1200 1260 1320 1380 1428
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- (2) INFORMATION FOR SEQ ID NO:264
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...455
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264

cggctcttc ttggcaaggg gcagacttct tcggcggtca aaaaggactg cgtacggcaa ttggcaacta atgcctattc ccagaaaaaat agttatggc gggaagagag attttggcta gatatcaagc gtgggcataa tctacgggga ctgttccgt	acgctaaggg tcctgtagga cttatatttg aacaagataa aactccttac gatggctttc	gattgtgeea gtgettttge agggeacaat aagttettet gatgegeaaa ttgaaaagta	ctctgtccgg aaataataat gacaggagcc gtctcgagat	ctgttcctgc cccttacaga ggcacacgct ttccgtttng	60 120 180 240 300 360 420
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- (2) INFORMATION FOR SEQ ID NO:265
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 586 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265

cgtcccttta	ccggaaggaa	tttcctatgc	cggttcgtgg	cagaagataa	acggaaggcg	. 60
gaceteetge	accytacctt	tatggcggat	gcggggtgag	cgacctcaag	gctttcgaag	120
cyacticaag	gcatattccc	catgatgtgc	tttgcatgcg	gctaattcca	cacccataca	180
ttatetecaa	ttattcaaca	cgcgcattat	gcgggaggag	aatggagcaa	tegeggaace	240
aacggatcga	gggggccact	tccacggcaa	tggggttttc	cqaaqtatat	tecgaaceae	300
Cetttegatt	acgggagatc	tgagttttat	gtacgattcc	aatctttgtg	gatgccttat	360
graaacggge	ggatacgggt	aatcgtgatg	cgaacggagg	aggggggata	ttccgtttta	420
cccccgggee	ggattetttg	aggaattgga	gacctgtttc	gagactccgc	tegaagttee	480
cycaagggaa	rggccggagc	ttacggatgg	agatatatga	aggccgtttc	cgccgaagac	540
cggaaacggt	gttgccttcg	tttttcgcat	ccgcgacagg	cggtcc		586

(2) INFORMATION FOR SEQ ID NO:266

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...544
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

```
ctgaatgtgt ataaaggaat atatcattga gccatttata tctttcattt ggagtagtaa
                                                                        60
tgttcctatc attacatgac ggagcataaa ttctttttgt cttgtcttaa tgtatcatta
                                                                       120
gctacaaagc gataccgtag acttgaaaac tatcagcgaa ctgccaatat tgtttgaacc
                                                                       180
aagagtggtt attatagtta tagceteatt tagtaaaaac cacateattt gatgaatttg
                                                                       240
caggcaattc ttgactttga caactggtta tataagactg atactatatc attattcgat
                                                                       300
gtaacagatg atgtccatca tectetetga tgaaceettt tattttetaa gtattgcaae
                                                                       360
aacattotoa toatataoaa etggeggtaa aactoattat cattetggtt ettataatoa
                                                                       420
tcaccctgtt gtacagttat gatgaaaaca cacttgacat ggcatcaata taaagttgat
                                                                       480
gattgntttt gaatctgcat agattgccaa gtcaaaaata tccataatgt tggatttgta
                                                                       540
attt
                                                                       544
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...795
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267

agaaaggctg	toggacatat	gcctatcggc	agctctttcg	ctgtagttcg	aggcaagact	60
cgaacttcga	cctttagatt	atgageceaa	cgaagctaca	ttgctccact	ccgcgatcaa	120
ttataacaca	aaggtaatcc	tttttgctaa	aaaccaaacc	gaaaaagcaa	tatagctcca	180
atttctaata	gtaaatcaac	acaaagagaa	aaacaaagac	cgattaagaa	gtacctctaa	240
accectate	aaaagtttat	ttctatatta	caatgaaata	caaacaattg	agtcgaggag	300
taaagataga	tgattgatcg	gctcttgaaa	cagggtaccc	cccttctttc	atcgctcaaa	360
caaagacaca	tgaccgaccg	cateteeaac	agcgtatcgc	atttgaaagt	ttatactgta	420
testtesest	ctttcttcta	tatttgggac	totogcacat	taattcgtac	ttgtttgata	480
accasatata	caatcattta	gtttataagt	gtgttaacag	ttcaaatgta	attgtcctga	540
acceagegea	addaaaccad	gactgacgca	ttaaaaacag	ctttctaata	cttttatagn	600
gedaagegea	agguactagtta	totatcatto	tctatttaag	gcctntgcat	gggttccgga	660
egicaaagee	aggtagee	aattatctct	tgatttttac	tactaaatca	tttcctctta	720
ceceggatag	agegeaaaaa	agtetgeget	tgaagatatg	ccgaggaata	cgaagaagaa	780
		ggcacgagac	cyaayacacy		, , ,	795
ttgaaagcta	LCCaa					

- (2) INFORMATION FOR SEQ ID NO:268
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...533
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268

```
60
ccccggaaac caattggcat gaacattgaa aatcgacata aaaatcgacc ctgaatacag
                                                                      120
cgttcatgga gtatttcatt ttcggatact tcttcgatgc tacgatcttg ccatcggcag
gtgctacaac ggcacggtcg tcattggaaa ggggctgtgt ctcttaggac aacgaaaaaa
                                                                       180
gttgatcgta agcagaagag gaaaatggca atgatcatta ccaaatagga tacaatagaa
                                                                       240
gccccagaaa ataaaacagg cttaagcata tccccgtgaa gagggttgcc atggtactaa
                                                                       300
                                                                       360
aagteeggtg etetettat gaacetteat gtegttetea teaagttgaa atgaateetg
                                                                       420
tgggattgca cggaggaaga gtatgccctt ccccgtgttc actaatacaa aagtagcgtt
                                                                       480
ttttctcatc ttcccgagcc gttgattatg ctccgggccc gtgagaatgc tgaaaattct
                                                                       533
tttaagatta agcatacgcg acagattggg aaatggaaga ttcgagatgc aaa
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{15}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269

tcgaccgcaa aggagagcag cgcttccgga ggatagctcg gtaccttggc ttaggcaatg ctggggcagt	tcgtctttgg ctcgatagac cgattgccg acgtattgga atcgcgcatt agggattggt tctgacggct atggtaccca	gcttcgcca cgtgctcccc gtcgctcctg aaaatgtggt ggcttgggga ggggctttgg	taatggctat gtctatacgc tttgggctgt tgtcggtcga caaagtatcg tctattataa	gatcggactt	gcatcagcat ccgttggcga tcatctttgg	60 120 180 240 300 360 420 480 540 600 615
--	--	---	--	------------	--	--

- (2) INFORMATION FOR SEQ ID NO:270
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 614 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{14}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270

ctcgccacta attttgtaat	cccttggtaa tgtcctgata	tgaagaagtg	ttggggatga	gcatgcagtt	atattgaagt ccagatcaga aagtttgctc caaagatagg tctgggaggg	120 180
--------------------------	--------------------------	------------	------------	------------	--	------------

			1/4			
gagaggggtt tcattaaaaa	ggatatgtat tacgtgccaa aaaaagaacc gcttttccgg	aaaagttttc	aacaacgaag	acgagtttgg agagaaaaca	ggetttaggt cateegeatt aatgatteta ggeteettgg tttgattgta	360 420 480 540 600 614

- (2) INFORMATION FOR SEQ ID NO:271
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 685 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...685
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271

ctggcctata gctttaccga tatggcctgg ttaggccggt tgggtagcag tccgtggcag 60 ccgtaggtat tgtggcggta ctgacgtggc tctccagtcc atatcgtcaa tcaataagac 120 cggcagtgag gtgacgatag gccacagctc ggcaaggggg ccatcgagga agcacgacga 180 tacgettege acaacgtteg atggteecta etggatetee teegteageg etettttgtt 240 ttteetttee cacacetttt ecteggtata taccatttgg aggacgatgt acacetttgg 300 ctcttaccta cctgcgcata gtggcatgcg gcctgccttt cactttgcag ccaccgcatt 360 cagoggtate tacaacggag coggactcag etcataccet teaaggtcag tagcacgggg 420 ttggtactca atatgattct gatcccttgc tgatattcgg tttgggatgg gggacgatcg 480 gagoggocat gocacgotga togotcaggt attogtatto gttotattot tttacaggoc 540 agacggcagg ataagctgtt ggattgcttc ccgttcttcg tccgaccgac aatataccat 600 ageggtegea tettgegtat eggeetgeet gtagetgtet caacteetet tegecateat 660 685 caatatgatg cttggccgct ggctt

- (2) INFORMATION FOR SEQ ID NO:272
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 920 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION $1...9\overline{20}$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272

cccccggttt cggacaaaga agagattgct gctatttttc cccgcacatc ggcttgccgc ttatttettt egeacetgga ggagagegga eggagtatet eetaegaatg tgggggttat 60 cettteggge ggacaggete egggtggeac aatgtgatag ceggtetgtt egatgagatg 120 aagctgctca accccgtagc cggctcttcg gatttcttat gggaccggat ggcctgatcg 180 agcatagtat cgcgaactga ctgctgaggt aatagatgaa taccgcaata cgggggcttc 240 gacatgateg gateeggaeg taccaagetg gacaageeeg aacgttegaa geeggaetgg 300 agatattgcg agagttggac atcaaggcat tgtcatcatc ggtggcgacg actccaacac 360 caacgeetge atectggeeg atactatgee tegategatg eeggaataca agtgategge 420 tgtccgaaga gatcgacggc gacttgaaaa acaaacagat agaaacctcc ttcggcttca 480 cacggccgcc anagtctata gcgaactgat cggtatatcc agcgcgatgc aattcggccc 540 ggaagtactg gcacttcatc aagctgatgg ggcgttcgca tctcatatta cactggagtg 600 egecetecag acceaececa atatettate gtateegaag aggtggagge caacaattae 660 tatctggacg atgtgtgacc tatatcgccg agaccgtggt gcgtcggtcg gaggcaggaa 720 tgaatteggg aceggtactt gatteeggag gggttgateg aatteetgee ggeattgaag 780 agggtgatca aggagctgaa cgagttctct tccaaatgat gcgaattcaa gcttattcaa 840 acgttcggga cagagacccg 900 920

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1996 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{9}96$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273

```
caactgcggc ctgccgtatt atataggtgg gtaatcaaag agagagaaaa tcttttcgtg
                                                                       960
cagacacccg aaaaattcgg cgactgctga acttggatgt tcgggtacag agtgaggtgc
                                                                      1020
tgtccatcgt cgctccgaca aacagataag agtgcgcgaa gccaatggta gagaatatgt
                                                                     1080
gagcactatg acaaattgct gctttccccc ggagccttgc cttttgtcct ccactgccgg
                                                                      1140
                                                                      1200
gggtagatag cccgggagta ttcacgctac gcaacgagag gatacggatg ccattaaaag
ttatttggac acccacaagg tgaaagtgcc atcgtggtgg gaggtggatt tatcggcttg
                                                                      1260
gaaatggccg agaactacat gcccgaggca ttgctgtcaa tgtcatcgag atggctccac
                                                                      1320
aggaatggca ceggtggatt tetegatgge aacgategtt catgeceace tgaagaaaaa
                                                                      1380
ggtattggtc tctatctggg caaagcggtg aaaagtattg aaaacgggga gaagtattga
                                                                      1440
etgetteget tgacteggge gaaaaaateg ggeegaaete ateettetgt etateggagt
                                                                      1500
gegteegaat aegaagetge agetgatgea cagttggeta teggaeegge aegeggaate
                                                                      1560
cgagtgaaga atacctgcag acatccgatc cggacatcta tgccatcgga gacgccacga
                                                                      1620
atacccacac cetettaceg gaaageegtg gaccaattte etggeaggee ggecaategg
                                                                      1680
caagggcgca tcgtagcgga taatatgcat ggacaacatt gcggagttat gaaggagcca
                                                                      1740
taggaacage tattgccaag atttcgatct cacggttgca gctacaggtt tgccggcaaa
                                                                      1800
ggeteteaag egeaaggeet teeetatgag teagtgaegg tacageecaa eageeacgee
                                                                      1860
ggtattatcc caatgcctac ccgcttacgc ttaaaatcac cttccaccca ggagcggtat
                                                                      1920
getetaeggt geteagtgtg taggeataga aggegtggae agegaataga etecateget
                                                                      1980
                                                                      1996
 caaatcatca agcgca
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{1}18$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274

` '						
ccaatcaata ccggccaaaa ctacgatcag ttgtcggcta gcttggtcag cgtctcatgg gcagaagaaa aagtagccga caccccaata ccccatattt taaaagccca acactattat	caaaggacgt ttccgaacag catactccgg gcatcgacat gcaaaaactg agcatagcgt ctgtcagttt tcgtccacat cctccgtata ccgtaaacga atgagtaaaa aatccaagat cgatctcacc ctatcatgt	acccegtcat aggegaacgt cacaatteet gaggggeaaa ttttggeega ttttgeteea ccacgacaga ccgggettte agtettatte atceteegga aaacteeece caatteeggt acaagaaaaa tttaacaaaa cataegegae	gtatttccac gccaataagc gcgattcagc tcggcccca tggagtttgg aaccaatcag atgttcgatg tcactcataa tcaaacttaa taagggagga attgcaagac actaaaaaaa aactattatt	ctgcaaccac atgatgatct gtatgcatca tactagccca ccatgagttc agcaatagcc acacgaacga taatggcaaa aaacagatga ggtttccgtt catcttaacc tatatcatca atgtagtaga acatttcttg aaatagcggc	tcgatgagag gtgggcaata gcacggtaga tgaccaccgg ttcgatctgc tcttcggcca	60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1080

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 548 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...548
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275

ctgggcaaaa catgacgaaa cgatgagcta ccgtgccgta ccaggtgtgt gtacaccaat 60 cccgaggtcg ccggtgtggg agagacggaa gaatcgctcg caaagcagga cgtgcctaca 120 ctgttcgtcg ccttcctatg gccttctcgg tcgatttgta gcagaaaacg aacaaggcaa 180 tggagagtgc aaactatact tgatgaagag aaccgcttga tcggagcaca cctcattggc 240 aatccgccgg cgaactcatc gtaaccgctg ccatggccat cgagaccggc atgaggatcg 300 acaaatcgaa cgaatcatat teeetcatee gaetgtagge gaateetaaa agaaactete 360 geoggaggtt gatactettt etgecetttt etaggaaate aaatetaaaa agteegtgea 420 gtcaacaaaa actgcacgga cttttcctct cttaatatct ttttctcaga gtattcggag 480 taccttcgaa gacagcaccc gaaaaacgag acctttggaa aataaggaga tggaggaaaa 540 gacttaaa 548

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{48}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276

tcatggattc	aacataaacc	agaagtacgg	ccacgttcgc	gagtcagttt	gcagatagcg	120
tactatcacc	tattectace	agegeattet	tctacctgtc	cgtacagggt	agccagatca	180
atanggatas	ggaaatggta	gaatcccgaa	gcatctgctc	ttcaacaagt	gctatcgctt	. 240
accagggcaa	tatoatttat	taaatacttt	taccctaagg	cgaatgacgg	gaggagcgaa	300
gagaagttgt	cycogcccyc	tatastasco	aataccataa	aatctgtccg	atgtgaacga	360
tectgeegta	agateetgte	cytyatyatt	tacgoogogg	cactcatage	cttgatgcag	420
gcagtttggc	caagtcgtac	ectyteggaa	tacagattaca	cgctcatagc	caaacgataa	480
catttcggcc	getgtggeat	atcetgeata	tectogea	acgetgeece	acttcaagaa	540
gctaccgcat	gtgaggatcc	atccgtacga	teettiggta	gacggcaaaa	gettegggag	600
tegteecagt	tcgctgagac	ttttggctcg	gaggtgtaga	gettgetete	tttgcaagct	648
ggaactgtcc	gccaagccaa	aagccttcgt	ataggcctat	ggtccatg		040

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...429
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277

gtaaaaacac	entetnacna	agectgaace	acagacatca	atatcttcaa	ataagaaatg	60
gradadacac	aguacyacya	agotojaato	daaaaadaca	tcagcgccag	ctcaaaggca	120
aaaaaagaca	gegtaattt	egatetgate	gaaaaagaca	etacenacta	taaataacta	180
tcgagctgat	cgcatcggaa	aactttgaag	cgaacaagu	acgeangeea	ttatasata	240
tatgaccaat	aagtatccga	aagttatccc	ggcaaacgct	attacggtgg	ttgtgaagtg	
ntagacaag	cgagcaaatc	gccatcgacc	gtatcaaaca	actctacgga	geegatggge	300
caacgtacag	cotoectcca	dadcacando	caatatggcc	gttttctggc	ttgcctccga	360
caacgtacag	Coloacicog	gagoaoango	annanagana	aggacctate	gcacggntca	420
agcaggcgat	acgttcatgg	gaetgaacet	Chacacgging	ggcacccaco	904-99	429
ctcgtcaat						10,

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 650 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{50}$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278

cagaaggtgc tcagtatcat gacgaagaat atgcccaggc aggtgctacc tggtagacgg agctaaggcc gtttatgacg gtgccgaagt gatcctcagg taaaagagcc tttgttcaac 60 gaacagetca atacgcacga agtagagtga tgcgcaaagg tcagtatctg atcacattca 120 ttcatccggc ttcaccgtga acccacgaaa tggtacgcaa tctggccaaa cagggtgtta 180 tetegtgact etegatggta tececegtat eteaegtgea caaaaceteg aegeetgact 240 togatgagta cttgtgccgg ctacaaaggt atcctgatgg ctgcgaagac ttcgccagct 300 tcatcccgat gatgggtacg gctgtcggta tgttccgccc gccaaagtaa tggtgatcgg 360 tgtgggtgtg getggettge agetttgget aeggetaage gtetgggage cateaettat 420 480 getgeegata tegecetgea getgeegaac aggeteagag ettgggagee aaategtggt 540 accgaccgtt cetgeegaac tggetatege egaaggegga tatgeeaaaa atggeeegat gatgtactgg ccaaagaacg cgaagccctc aaggcacatt caggatatgg 600 650

(2) INFORMATION FOR SEQ ID NO:279

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 655 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...655
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279

cccctggagt tettetatga teattetegt tggggtaaga tagagggtga ggaetgtete gecettetgt caaacgaata ectaetteeg tgataeetaa agagteggta eceteatatt 60 gtgetttaac tetatettat aaagacegaa tagggaaaae gtgeggagat eggeaggega 120 aaccggtttt getgetggea acceetttte egtteeactg ttgeggettg teggecaaag 180 240 tcagaccaca gagtccgcaa agatcagacg ctctcccact gaaacctcgt atgcaatgcc 300 aaatcgcgat attcataccg attgtcatgg cggatcagca gctcaaagaa tatgagcgag 360 tatagtccgg tatgaggatt tcgtagtcga gccatcgcgc ttctgccacc ttccatgagg 420 cacctgacga tacagtatte gtegteetta engtatgtge aagacacaag ceaagcatat 480 ccccaatgca ccagaaaaaa actgattgcg ccttcggact tgctttcgta ccggcaagcc 540 ccateteect ttatteette tttetetttt eetggtegge tttetgaetg gaagtgettt 600 gaccgcggtg gtctgcgca ctggccacca cacgtctgct tctttcatac gttcg 655

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...3\overline{03}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280

agategeteg cateteggae	tttggctcgt gaacaggcca aggcccaata	cagcacaatg aagctatttg gacaaaattc	atgccaactc aaaatctatt ccatccggaa	ctctcgctgc tggagacgcc gtagtactta	tggactgagg ctgcacgctt ttttgaaggg acccaacaaa ggaagaccat	60 120 180 240 300
aaaccagaaa cgt	taaagcaatg	aatategata	accecede	aacgaccag	3 3 3	303

- (2) INFORMATION FOR SEQ ID NO:281
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 617 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...617
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281

ccactccggc ggcagcgact cgttgtctct gaaacctggc taggtaagtt catcgacggc tcgtcgtcgc	tgtggttgcg gtggctgtca aaaaagaatg ttgaagttga attccggctg tgtccggcag ccagggcagt cctatttcgg	gttgtagctg ctgatcggac gcttggagct gaatgtcaca actacattcg ggctttttgt ccattatact ggagaaacca	cggcagaaga cgaaagtgat aaagcaataa ttttaatttc aacacagcta gagaatccca agcatggaaa tctccccggc ccggtgctcc agtctcagct	catcagatgy aacggagaaa tcagtatctg ttataaatca cggaaagcta ccatcgagcc aggagagtga tattgctttc	agctccaaac ctctttgtca gatgatacaa tcggaggtgt gagagttact	60 120 180 240 300 360 420 480 540 600
ttaaagatgt geegactata	acgttctgct	gactaccgac	agtctcagct	tcattcttcg	teceggacat	617

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 712 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...712
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282

cccgaagagt tgaataagag aatcgtctac ctcggtggag aacgacaact tttcttatgg 60 atcttatgga ggtaagtgaa gagaccttca aactcaactt gagagttcta ctcttacgag 120 cgatgagaag cactacaccg tggtactcta tccgatgcta tgattgaacc taagctcctt 180 gagggggtaa aatttgaagc acggaggtga aagactttgc ctgtttgctc actcatgtag 240 gaacagcagg ttctacaaca agaagaagaa aagagaggaa cagaacatcg aagagttgaa 300 acggetetaa gteaceaaca tgaactatae geeagaggtt eeggttttae ttegataeta 360 aagagcaagc aaatcaattc tgtgaggacc tcagaaggtc cccaacttcc ataccatcgg 420 ctacaatcat gctatcatca tgaaccaaca aaaacaaaaa aataacaaca atcagaatat 480 gaaaacagca cttatatgat ccattgcctt accaatatgc atgtgggtaa gggagatgca 540 cctacgaagt ggtggacaaa tgtgtacagc gagatgtaac cacagggagc cctgcatcta 600 ctcctccage ctcaaggage tttgagacag ttcttttgaa acaaggettt geegagetta 660 actattgttt ttgggaagat cagagegggt tagaaaaata tggcatgaga ag 712

- (2) INFORMATION FOR SEQ ID NO:283
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1001 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1001
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283

cegeegttetceacatageggatacgaecacetteggattgttgeagggeaaagecaagg60aaageegaatggtetttacegtgaggatteteggeeggaecegtettgeeggcatacete120tattteeceeggggegaagttggetgetgacaggtteegecegttaeggetetegeeatt180cettetactatatacteatattegeeggaetgatgeegetattetgeeagttegtataag

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 619 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...619
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284

atasstaas	ctatggcgtt	taggaaggac	ttcaaaggga	ggaggtaaag	tgcaattccc	60
Ctyaaatyya		assassascc.	cctttcatat	tatccgaaaa	ggggagagaa	120
tgaattatat	cggiaaalal	gaagaagacc		gagagattot	ttcactacca	180
tcctttcgat	gtccaagaac	gagtcagaga	ttttgggaga	gagagacccc	11 15	240
agcagcgtca	atcaagtgtt	atagtgacac	ataaaacaac	aggtagaata	ttatigaaca	
atattaaaa	ageeggest	cctcttttag	ggggagacag	atggataatg	cctcgttgca	300
acycciayay	ggaaaggaac		atagnatata	agataatcga	gtatttctct	360
aagatctctg	taaaactagg	aattgtagaa	gtcgagtatg	agacaacega		420
cttaataact	gatattttaa	tggatattca	aagatagcga	agttcttcga	geagttgeaa	
antonnantt	ftactcaata	gaggattgtt	toggtaaata	tgacgttgaa	ttttctgatg	480
aaccaagacc	cegeeedate	agtastatas	tcatgttgtg	ttottcaata	acagactcac	540
atacagctga	actititete	ayccacycya	ccacgeegeg		gaggeteata	600
aaagtcatgt	tgctcaaaac	atcagattcc	atactgtcaa	ceggeggeee	Cayyeteata	
atagggggaa						619
acagggggaa	9					

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 556 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...556
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285

			ccggagcaat			60
			atcgagtata			120
gacagggcca	catcttcatt	ctcatagctt	cccactgatt	gacttttaag	gattcttgcg	180
atgtatgcga	agcggagaga	ggcttcttcc	ccagccaata	gagactttcg	agcgtccgta	240
cggagtcgtc	ccaacggcaa	cgatgctgcc	ttgccaatca	cgcagggctt	ccaggatgag	300
cgctcaatga	ctatcagttc	acggtgcatc	cggtgttcac	cgaagtctcg	cttttgacgg	360
gacggaaagt	gccggctccg	acatgcaggg	tacatcgaca	accggagtac	cctgtgctct	420
			aacccggccg			480
agatttttgg	atagacggtt	tgggtaggtt	tccaagtctt	cctcttcggt	atcccgatta	540
gatagggggg			•			556

- (2) INFORMATION FOR SEQ ID NO:286
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...515
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286

cctctcgcac	ccgtatcaag	acgctaacta	cagataccgt	actggctaaa	gtcgcttttt	60
			tgctctcacg			120
			gacatactaa			180
ctgtggaagg	tgcagtagcc	aaatgtggac	gatcacagcc	ttgcagctcc	atcgtcagag	240
tatcatgtct	gtgacgaagc	tgcctgtgtg	gagctgaaag	tgggcacgta	caacacttta	300
aggatatcga	acgcaacaat	ctataaaact	atgcgctacg	actagctatc	atcggtggag	360
ggcccggccg	gttatacggc	tgccgaacgt	gcgccaaagg	tggcctgaaa	accctcctaa	420
ttgagaagaa	tgctctcggt	gtggtatgcc	tcaacgaagg	atgtataccg	accaagacgc	480
ttactcttac	cggccaaagt	gctacatcaa	attgc			515

- (2) INFORMATION FOR SEQ ID NO:287
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...430
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:287

cgggcagaat gttcatgacg gccagcatga tggagagaag tgccgtcatg cccagaattg 60 aggecagtte caagaggeeg ggaaaagget geccaatgee egaagecace tatetgteet 120 geceettett tggtgaagae gtaettetgt egettaegta getgegeatg gtgeeeatae 180 cttgtgctat tccggcggta tggcttcgaa tagcgaatat cggatatgat cgatggtata 240 gatggatcca acggtcggag gctcactccg ataagtccgc cggtatctac cggcgcgtta 300 tagtcagete ttegeetget egggetatgg acagggetat ggttegeetg catggetgeg 360 aatggctccg atcacatcgc ttgcatcagg cataacttgc catttacggg agtgatactg 420 430 tegecegttt

- (2) INFORMATION FOR SEQ ID NO:288
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 672 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...672
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288

cagtaaaatc gtcatcataa aagagaccgc ccctgctcag cctcattttg tatattcctt 60 ataacctctt caaggggaaa cctctacctt tacggtcgaa tcaatttcag accgatggat 120 tacgaaatag agaacaacca tgccgacgta ttcgcagggg aagtatcgaa gtgatatgcg 180 240 getecatgtt cagtggaaga eggaagaget getaegeegt etgeggagag etaagatage 300 gcgccgacgg tggagatatt caagccgacc atcgatatac gctacgacga aacgatgtcg 360 tttegeatga caagaatget ategetteea eeeeegtgga caateggeea atataetget 420 gctatcctcc caagtggatg tggtggggat agcgaagccc agttctttga tgagggtctt gtggaagtag cccagcaatt gccgatcagg gtgttcgcgt tgtgatcgcc ggattggaca 480 tggacttteg egteageett teggacetat geegggettg tgtgccatag eegacteegg 540 accaaagtte atgeegtgtg tgtggaatge ggeegattgg eeagetatet tteegtegtg 600 tccaagcgat ccagcaagtg atgctgggcg aactgaagaa tacagtcccc tctgcagaac ctgttacagg aa 660

(2) INFORMATION FOR SEQ ID NO:289

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 946 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...946
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289

cccgggcgat tttccggaac atctgtatcc tttggagccg acgatgacgt gaaagaaggt 60 gecagagtga tgttegtteg caatgataet egecaaceag aegetaetae aaegggaaaa tageogtagt coactoott teteettete ggtggtegtt eggaetgaeg geggagaget 120 180 tatagaggta gagccaacga gtggaccaac gtccgctact ccgtgaaccc cgagaccaat 240 geocegaaca ggaagtaate ggeagettee geetttttee gettegagee gettggetat 300 caccytycac aagagccaag gactgacttt cgaacacycc gcctagatct ggaaggtytc 360 ttegtteeeg gteaggeeta egtageeetg teegtatgae gggeeetgaa ggaatgatae 420 tgetetecee teeegatetg etgggttgga aacteeceaa gaactggteg aatatgeaca 480 gacgaageee acgaaaaaga acteeggaet tetttgeagg aaaacagtet tatetattga 540 ageageaate egacgagget tttegactgg cagaagettg ttgaatattg geacaaacae 600 agtotoagot atogggagga gagogagotg agcagoaaag coattacago gatagagoag 660 ccgaacaatc ggccaagata gatgcgtcac ggaagtagcc ggacgttttc gccggcaact 720 tgeeggeett tggggeagte teegettgga ttnggtgeeg teaaagageg aategacaaa 780 gccgggacta tttcctgcca caactttctg ccatagcagg cgaactttcc tcccgatcca 840 agaagtegga atgetgaaaa aageeaaaca gtttgegaaa gaetgetega getacaggae 900 aatottoana cogoogtgta cogootgott cottacgago cgtttt 946

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...984
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:290

60 aggaaagatt eggacaaagg eggeggattt eggeettgea atgeteeaeg eegtetegta 120 getgeteatg gegtagtgtg ggaagagegg gaggaegaga ggetteggee gtgtggeage 180 tectteagea categgeeac ageeggetge egtagegeat ggetacatgg aettetetge 240 ccgtatgtgc cagtgccggg ctatggcttt cgtatgcgat atgaggggga aagaccgggt 300 getttgteee aaacggteeg atatttttgt geegaaettt tetttetgaa aggatgatga tacctctcac gagtaactgt ctcaggagaa aaggcaaggt gatatcctcc tgtcggtcag 360 420 aaaagaattg aggtagegeg ceaegteett eteteaggge tgteeggega geegatatte 480 agcagcaata ccacctctct ccacccttat tgtcatcggt tcttctacga tctgccataa tttcaggacg agataggtaa gattccgttc gtgtctctta tttttcccga tcccattctt 540 600 aaatgaatga gagcattaac ggagtaagga agccgtattt gccgaagccg gatgtgcaac 660 gaataaaggg atcgactctg cggcaaaagg attcgacaaa aggccgtgcg acagtttcac 720 tctctgcaag ggatatacgg gtacttcggc aaaagaggga atgtccgaca ggaaatctgc attgcgggcc gaaaaagtcg ctccaagccg gaggaagcat tttccgcgcg gatttgtcgt 780 840 cctcaagttg gagcagtgaa tttcgtgtcc gatttgcagg tttgcacgcc gaaaatgaca ttttcccgac cgaaaagccg tggagacccc cggattttgg agggttggaa gggtcggctg 900 960 tgggtattcc tgtgattttt tactcccgat gtatggtttc actcccgacg acacgctgaa 984 aatcatcggc tcaaaaaccg tctg

(2) INFORMATION FOR SEQ ID NO:291

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 878 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...878
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291

60 gacgtgtaac gttcgccgat cgagccgtca ttttacttcc aaaacgggca tgaggctttc 120 ataaatatca geeggtgtet tggeatagag aaagaeggat atetgttete agtetegtaa tgattgccct cggtcagggc tgtctgatga gcagattgtc atcctccgtt tgaagaatgt 180 240 agaggtaatt gaagtaccct gtttcatcat gagggtacga gtgtacatct gctccgaagc 300 atcatgaaaa getegegtte geteateggg agaaaatega aageetetee ggacaaagga 360 ccggccccgg caacttttca ctctcgaaag agaagataac ctctaatagt ctccttcggt 420 agcactatta gcaccategg tagtacgaat gaacgtetae egaaattgtt ttgttegaae tgatagggta atccggctct gttttgtcgg gatacaactc catcacatag tgcccgttgc 480 540 gcgagtaaga cggtacaccc ccataccatt gtaactatcg ctgagcatct ctgccttccg taaacattgg ttgccggaaa taaagctccg gcatgctgat catatacatg gtattacctg 600 660 caatactcga aggtccggag agcgaacgca tctcggatcg cgcccgtttt gtcccacgac 720 aagggtaagc teeteegagg gggacagate egtaageeet teagatetae eteaacattg acttgctgat gacgacgtgt atatcttcat aagtaaccga cgtttgcaaa cccttgaggg 780 840 aagcaacgga actaccacac gaaaggcgat cgtaagaagc gtttcgtncg gatataaacg

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 581 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...581
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292

gcagtgetet tteccatgag tacttetteg aatgetegga gaateaggga egateeagag 60 aatcgcccgg catccgtccg gtatagtcat tgaaattttt gctccgctta taccgaaagc 120 gtatgccaca gagtcagcag aagtcacata ggcttcacgg tttgcacctc atcctttttg 180 ggcggttttt ttgcaaggca gataatccgg ccactaaaaa ggctaagccg gcaatgatca . 240 ttacttette atagtgattt gtettetgat tatttgttga taeteaataa ttegttataa 300 aaatgagegt actacceggt ttgatatgtt egeeggeace aegteteeat aegeeagate 360 gctcggtata gttactttcc acttggatcc taaggcatta attgaagaat ctccgtccag 420 ccggctataa ctcctcttag aggaaactgg ccggttctcc cctgtccata gagctatcga 480 aaacgatacc ttgatgagcg taccgtgata atgacaggtt accgtgtccg aaagggtggt 540 ttcgggccct ctcccatctt aatgacttcg tattgcaagc c 581

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...766
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:293

taacagtgca tggcagattc ttgccctcgg cactgaatcg gatgtcattc cgattttctt 120 180 tootaataaa ootggoattt cagttttatt aaaogtttot caaaotttga tttocaotto , 240 cacaccgctg gggagtccaa tttcatcaga gcatccacag tcttggcagt agagttgtaa 300 atatcatcaa tetettgtat gaagagagtt egaaetgete aeggetette ttgttaegaa 360 cgtagagcgg ttcactgtga aaatccgctt atgcgtgggc agagtatagg accgctaacc 420 ategeacegg etgettteae egtetttaeg atttetegge agaettgtee accageatat 480 aatcgtaaga cttcagctta atctaatctt ttggctcata tctatgttgt tcttttattt 540 gatcaaatca cgcgaccctg agcttcggta agcacctgct tagcgatggt agagggcact 600 ctgaatagtg agagaaggtc atcgtactcg tagcacgacc gctcgttacg tacggagagc cgtcacatag ccgaacatct cagccagagg caccttacct ttacgatacg tgctccggta 660 720 eggetgettt ceatacette cacetgeeeg egacgettgg teaagtegee gateacatea 766 cccatactct ctttcgagtc accacttcca gtttcataat aggctt

(2) INFORMATION FOR SEQ ID NO:294

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1781 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1781
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:294

gececattge ettgegaagt tgtaggggtg tattgeegag eatettgege agaaageaea 60 120 gaggtageng neagaggaga agagattett tteegetatg eettgagaga eagagaegga 180 teggecaagt etgtgtagae atgettgeee tttetteatg catecatttg agtggeggae 240 aactgaattc ctgattaagt gacgtttgaa agaactgagc gacagattca ttttggctgc 300 aagetttetg eegateggea etecaaatgg tgteggaata egaaageaeg aaageettgt 360 tctgacagtg gaatgaggag agaaagttgt ctaaaagcgg ctttcgtagc gtgagcggaa 420 gatgcagaag agttcgcgca gtttcagctc gatatctcgg acgaagtggg catttctgac aaatatccca tcacagagtg ggccaggagt tcaccattgt ctctcgttgc aaggaggaga 480 540 tgtgaacgat tcggttcgtc tccggcattc tttcttattg cccgaagagg gacaaatgcg 600 aggcataaat ggagcgtggg atggaaataa aagcaaatga gcgtagccgg cctttttcag 660 ctctaagtct tatacgaaga ttggcagcca aaaggacaca ttatctcccg acaattgcga attaccggat tccggcccga caaataggcc ggctctcctt tgagcaggaa gagcaaagca 720 780 tggctgtctt tggtcagatt tccaaatcag ctccttgtcc taccgtgtgg agttcgggca 840 atccgacaga gcagtggtcg gtcggctgtt gttcaggatg ccattcggat ttttttggga 900 gagacagget gacagatatg aatacteata aggaggatgg teggegttat etttggeaaa 960 gegagetatt atgtgaegag etgeettgte eaggtattgt eegtaeegat gettttgegg 1020 atggagtcgt atccggacaa tgtgcttgtc gctctgcgga cgaagcatca aggagcggag 1080 acaaacttgg gccaaccttt tctccgtgaa caaggetccg aaaagttcgg gcactacacc 1140 ctgccggcaa tgaggttggt cagcgaaata aaaggcgtac caaagcatac ttgaaaatca 1200 gattggtcag tcgaacntcn tcgaatatag tagcatcgga cctgtggcgt accgatcagt 1260 geggtttega gegtageegt teetgagtta egagggetge tttgetetet eggagtattt 1320 catacgtgcg tccgatacaa cgggaatgct gtcgtcgggc aaaaatggag tatagtcctg 1380 tatgtcagtc cgggtgcacc ggctatgaca gggcggtagt ccgggaattg ctcatcacac 1440 gcagcatcac aggcaaattc tccttcactt cgagcaagcg attccacaga gaagggctac 1500 ttgacgagaa tctttggctg accgctcttg tcttcgatcg taggccgcat gtgttgcttg

acggcatcat agcacggatg co	ctacataga tga	caggaaa atcgtgtcc	I gcaaaaaaat	1560
ctttctcgaa ggcaagatgc ag	gagcatgag ato	gacgtat ttcttcaac	tettaateae	1620
caggatttcc atgcccagac ct	ttaggagag ata	taataga ctategette	ccaagetett	.1680
egegtacaaa eggaagtaeg ta	agcgcatat tga	ageeggg tagtecacto	caataacaac	1740
gtcggggtta aatgctcgca to	ctgtcctgc aca	tgttege e	Jangabaa	1781

- (2) INFORMATION FOR SEQ ID NO:295
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...409
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295

aagaccacga tgaacgacat cgccgatgcg gcaaacaagg gacgacgcag ctatatactt 60 acttcaaaag caaaaaagat atctatttg ccgttgtcat aaggagctgg acgaactcta 120 cagctcgttg gagactgctg ctctcgttct atgccgccga ctaagaagct gatgcacttc 180 atctatacgc atttggagca atcaaagaga ttgtcgtgcg caatggtacg cttcgtgccg 240 aggttgtcttgatct gttccatttt ggacgaaggt gttcggctta atggtttct atacccgata 360 cccatattac cgccaagac ttactcact catcaagggg ctggaagtg

- (2) INFORMATION FOR SEQ ID NO:296
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 669 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...669
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296

atcacattat	aaatgatcca gggagtaccg gtgctccttc atcccggctg	tacggcaacg accetcatge egeettgatg ggacgtgage	ttttttcgac cgtgccatcg tgtcggaggg	aatcgtgtgg ctctgaatga tgagatcagg	ccgttttgat tattcgcatc cagtcgagac	60 120 180 240 300 360
atgetettta tggaaagggt attegattae	gtgcttgtgc gaagagggta atcggaatga tctgctgttc	agaggteggt ggaagttget egtaggeaaa geteteaaga	cggctatgct cctacgggca acgagcagtc	ttccaggeteca ttccagatca atgatatacg tgcgcttcag	gaaaacagcc gtagagattg gagacgacat ggaagggaaa atcattgctc ccttgccata	420 480 540 600 660 669

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 592 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...592
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297

ccagacaaat caacagaaag agaatctcgg acaggcatag agaatttgaaa ttgatgtgt gcaacatatc gccgtgcctc cgagaagtcttt caggatattc agtggtgatt cagacagaat acttcgatcacc gtatcgcatg gatcatttge gggacaccgt tggtaatccctc cggaatgttc agatcttca ccggtctttt gggacacagag tcggccacat cggcattggc cagcgtcagg catcatatcaag gcggtcagcc atgaaatgta gtctatattc tcgagagatgaa tacatcggtc tgatccaacc gggatgaca tcgagcgatgaa tacatcggtc tgatccaacc cggcttctat tggagcgatgaa tacatcggtc tgatccaacc cggcttctat tg	ccactacat ggtcgtaggg 180 gcgcaccat gccgccgaag 240 gtgacgggt gctcgcgatg 300 actcaccgt actcgtatct 360 tttttgttg atgagcgtgc 420 cttccttgg cgatggtctt 480 cgtctccga attttccgta 540
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 529 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...529
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:298

ggcgaaagaa acaccgcagg acgataagga agctttcctc ttcaacgtac ggttccgcgc 60 gtactetetg tettgggaac tegeaacece agtggttagt acegggtate aacaacatee 120 togaaggogg ctatgtaaag googatgoac tacogotatt coggtggata gtatgatgoa 180 gegeggaege agagegteat ggetettgae egactaeage aaggeeaaac aageeggega 240 catggagetg cectacagea caaateegtt atagaegaga attteeeta tttegetata 300 getatateca geacaagaac gacatagtte ecceegttgg getacetaet acagetteeg 360 tatcatggtg ggactcggta tgctgttcat ccgttattcc tcatggcatg gctcctgagc 420 ttcaaaccgg aaaaattcag caaatgcgat ggttccacat gatcgctatc gtatgtatgc 480 ctcttgcatg gtagccagtc agagtggctg gatcgtaccc gaaagtgga 529

(2) INFORMATION FOR SEQ ID NO:299

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{147}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299

gaactaaagg gcggatttaa cgttagcctt agggtcggac tgagttgcta ttgagagaca 60 atttegeegt etttategat acegggacat eegacatetg egeggeggee ttgeattgat 120 gtggtagcag aagcagcgta ggatttacgg aaggtatgaa gcctctactg acggtcgttt 180 gtgctattat teteetteet tgeetetegg tgggcagaeg gtggtgeeeg aatgggatga 240 atacaagcag agcagataga atcaggtgca ctcggggagg acgagggagc cgaattctgg 300 aacggtggat ggtgcagaag cagcatccgc tggacatcaa taccttaccc gggaggactt 360 ggagcaattc ccctttctca atgagtttca gaccgccgtt tcctgctcta ccgacatgct 420 catecegagg ggttegacag etttgggtge tgagtgagat tgeeggetgg gacagaegta 480 cctgtctgct ttgtggccga tgctgacggt gcagaagcgg agcgagtcgg ctgccgcctt 540 tttcgcgaga tcctgtctta tgcccgtcac gatgtatcgg tgcataccat gccatcctcc 600 agcagcagga gggctaccgt ccggatagcc ggcatcctat cggggcgatc cgtggggtgg 660 cggtttgcgc tggagctacg ctatggcaat cgtttttcct taggccttac tgcgtccaaa 720 gaccggggag aaccgccttc gataagcggc gaaagggctt cgacagctat tccgcccact 780 tettatggaa gggaaggggg etgtgegage egtggeacte ggagaetate gaaagggatg 840 ggatacggcc tgctcgtcaa tcaggcctct ttcatgggaa tgcctacgcc tatcctcgtg 900 geggaaceae getgegaegt gegtttaeet ageegaggae aactteatge geggggeege 960 taccgctctt gcacaaggac atgggcactg acggcatttt attcgcgcca ggggatcgac 1020 gccaccgtcc cgaagacggt gccatcaaag ccatttacca caccgggctg catcgtacga 1080

192 teegagateg egeggegaaa egetgeeaeg atgacaeega ageaettegt etgetataeg 1140 1147 acgatcg (2) INFORMATION FOR SEQ ID NO:300 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 226 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:300 gtgtcttggt gtatttcttg ttcagcagtg tgcgaatacc acgccaatca aaccggcatt 60 gatttgacgc aggaaagagt gtttcatgcg atctctgcaa cctgagtgta gacttgacag 120 180 tttgtttggt agccatattt atgctctgtt tatacgtgta aaatactaaa tattattgat 226 atacgcaagc aatgcagcaa atatgtcgca aaaatgccgt gcaatg (2) INFORMATION FOR SEQ ID NO:301 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 863 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...863 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:301 60 aacgacacga acatcaggtg acaccttgga tgcaggcttt ccgcaacgct acgagtggat 120 agccaagcag gtgaaaaatg gatgatcgtc gcccccaatg acagaggagc aactgctttt 180 ccgcatcgca ctcacgcatg taaaagggtg ggtagcgtgc tggcaaggca gctgctttcg 240 gctatgggca gtcccgagcc atcttttccg acaggaagga gctggtacag aggctaccga 300 aagcactcgc cgcctgctcg atgccatctt ctctccttcg gtcatggagg aagccgccga

aagttggatc aagccctcaa agccggtctg aatatgtatt tcacaccgat gataactatc

360

cttaccgctt	gaaagaatgt	gtcgacgccc	cctccttctt	tattccaaag	gcaatgtcga	420
			gtacngcgca			480
tcagccacgg	gcgaatcgta	tcgggattgg	ctgaaaccat	ccccgatttg	cttatcgtcg	. 540
cggactggcg	tacggcgtcg	atgtcgcagc	tcataaggcc	gctttggaaa	tggcttgccc	600
actgtagctg	tattggccca	tggattggac	aggattttcc	gagcggtcat	cgttccattg	660
ctatggagat	gctccgaaac	ggaggctgct	cacggattac	cctatgggga	ctgaaccgga	720
ncgattcaat	ttcgtggtcg	caatcgcatc	gtagcaggct	tgtcggacgc	cacacttgtg	780
atcgatcggc	cgaaaaagga	agctccctca	tcactgccgg	actggcattc	ggcacaatcg	840
cgaagttact	ggctcctacc	cgg				863

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 857 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...857
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302

gacttggagt ccgggcgaaa gagcgaagag gaattccgaa ccgagctatc cgatacatag 60 gaaaagaatt gacctatcag caggtgtacg atgctctctt ggttttcttg aggagatttc 120 180 ggccgaaaag ttcgattata tcgactecta cgccccgatt atcgactett cetectetee 240 aacaccaatc ettatgeete gatttggeea tgagteegeg ttttetteee teaggaagga 300 cgctgatagt ttctttgata aagtctatgc cagttgtcag atgggggaaat acaacccaat gaagatattt teetegaaat gatageegae ageggtatga ageggaggaa accetettea 360 420 togacgacgg accggctaat gtggcaacag ccaacgactc ggtttccaca cctattgccc cgacaatggg gaaaactgga tcctgccatt actcgactcc ttcgcgaaca gaaataaaga 480 agggetgtac gegaategtt tegeteegta caageeecet tttegtateg aaagaacgtt 540 600 gettattteg taggetettg categtgaag tecaegttea gettattega tecagteegt 660 accagttgcc tgtaatagca tcgatagcca cgggaataga ccaccgagta catcoaatac 720 cacccactty gcttccacac ggttgtgatt atacgtatga tgggctgttt acccggaata 780 cgaaattcca cggtgaggat ttgtcagcct tgagcgagag ttgcaagggc gtttgtccca 840 tettteacea ttgatgtaaa ettetgetee etgtgggttg gaaaceattt ceaageatge 857 gtctgtttgc cgaaaag

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...427
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303

cgatcagttg tccattcaag agtattgcgt	gagggaggtg aattacgggg acagcaatcg tcttctcttt	atatgataget gateageteg ecttegatge	gacttgggta tcaatgagta caaagtccgc	tcgggctgat tgaagagacc ttttcgggta tgccaaaagg	gcagaccttt tacaactcca gttgctcaat aagaaatact	60 120 180 240 300 360 420
	~~a++a+a+a	taccaactat	acttccqatc	Lyccaaaagg	gagaacatga	

- (2) INFORMATION FOR SEQ ID NO:304
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 596 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...596
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304

ggaagegee acgaattitt gtategtagg eccateegge eccatgical ggeteegas 36 ttggtettgg tetgaetete gaagacagge tetteeactt tgaactgata getgeggeea 42 tgeegetacg aatgtegetg tattegaaat tetggagtag aactetttga tegtaeggge 42	tgaggtggac	ggtgcagtca	cactcatact	ttacactcac	gttcgctctg	ttgggatcgt tagctcgttc ctggatcttg tctttcttca	60 120 180 240
LL -L octoberodod factdctdcd tallydylydc gwowlood	cgcagcatct ggaagcgccc ttggtcttgg tgccgctacg tacggcctca	acgaattttt tctgactctc aatgtcgctg cggaaagcac	teggtatgga gtategtagg gaagacagge tattegaaat tagatgegte	cecateegge tettecaett tetggagtag ecceettgtg tatgggtgae	cccatgtcac tgaactgata aactctttga tcgtattctg gacatctcat	ggeteegagt getgeggeea tegtaegge accgtteaca atccgtatee	300 360 420 480 540 596

- (2) INFORMATION FOR SEQ ID NO:305
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...377
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:305

gaccgtggta gcaaagatta tttttggagt aggtaaagtg gtttcgtcta tgtgcgggtc 120 aattccggac agtggaagtt gcattattct atcgcgatta tcaaggcagc gtgacggata tacccgaagc catgcgatac acagggata tacccgaagc gaagagttat ccaccgacta tgacggatta tcaccgacta tgacggatta tcaccgacta tgacggatta tcaccgacta tgacggttc 300 agtatgcccga ccgtcca 377

- (2) INFORMATION FOR SEQ ID NO:306
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...711
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306

taggcaattc gcccatcagc agtaccatcg aggaagaggt ggaaaaggcg tctgggccat acgctggggt gccgatacgg tcatggatct ctccacgggg atcatatcca tgagacgcgc 60 gagtggatca teegeaatte geeegtgeea teggeactgt geeectetae cagaegetgg 120 agaaggtgca gggcgagtga cgaagctcaa ctgggagata ttccgcgata cgctcatcga 180 gcaggcgagc agggtgtgga ctacttcacc atccacgccg gtctgcgttg gcacacgtgc 240 ctetgacett gegeegeete aeggggateg tetecegegg tggtecatea tegecaactg 300 gtgcaccacc cacaagegeg aaagtttcat ctcgagcatt tcgaagagat ctgccaaatc 360 ctcgcacgct acgacgtagc ctatctctcg gcgatggctt gcgcccgggc tgcatccacg 420 acgccaacga gctgcgcaga tagctgagct gaagacgctg ggcgaactta ccgagatcgt 480 tggaagtata acgtgcaaac cattatcgaa ggaccgggac acgtgccctg cacaagatcc 540 gegagaatat ggagatteaa etngaageet geeatgggea eeettetaca eteteggeee 600 gttggtcagc gacgtggcgt ccggctcgac catatcacat cggctatcgg c 660 711

(2) INFORMATION FOR SEQ ID NO:307	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 381 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1381</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307	
ttegteeaca tegtegeett eggggateae egtgatetgg teacacegge tgacaggaaa ggeteettet egeagagett ettaceggte agcacattee ategateaea egetegtgag atteettat tgteagtegg eeggggagga agcaaagaca ttgeaaceeg geataataeg gacgtateeg tgageteage gtetgageeg gteatggeaa teattetggt aaaategget ttgeegtaag eaggaaacgt eegateaega teaggteggt agcettgage gteecacegt ttegeeega ttgattgget teegtatgat tgateageae geeactttta eetgeeggat gaagteeegt gttaetteet a	60 120 180 240 300 360 381
(2) INFORMATION FOR SEQ ID NO:308	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 677 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
(Vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS	
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1677</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308	
gaccgatcgg atttcatctg gctggcttcc gatgaggatc gcgaaggagg gccatcgcat ggcatttgta cgaagcatta gggctgaaaa acaaacagcc aagcgaattg tatttcacga aatcaccgag acagccatca gagctgcatc gaaaatccac gagatataga catcaatctg	60 120 180 240

gtcgatgccc aacagggagg cgcgtcctcg accgtatcgt cggcttcgaa ctttctcccg

ttttaggaga cgtattegte ettetette ggeagggegt gtaeagteeg ttgeetgegt

240

300

gacgaaggag gacgttacga gcaggaagca	agagagageg cgtccttccc gaagcccgat gcgtccgggc gcccgaaaac aaggcttatc caaaaga	gacggtagaa attcttggag aaacgttctc tcggctacgg	tgtgacggcg caatgtatgg cggccactcc tgtggcacag	gaattgcaga atgcccactt ttttactacc accatgcgat	aacgattcaa tcatataaca tcgacgctca	A	360 420 480 540 600 660 677
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 631 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...631
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309

gggagcaaat	aggagataag	gatacqqaqc	aaacqaqaaq	cactattegg	aaacaaacag	60
aaagaagaga	cccatccada	atototoget		·	adacaacay	60
~~~+~+~+	- to the country	accectacce	creetgtgee	aagcggataa	agatttgacg	120
gagicicati	atatecattt	gggcacgtgg	acqatqaaaq	caagactacg	acasaastta	180
cagcctatcc	gttgaaaacg	acattataaa	*****		gegaggattg	100
taaataaaa		gegecatega	caaayagegg	grgcgagaag	tatcgactcg	240
cececeaaae	atettteegt	caataaaaat	ctqqctactq	Caaaacagat	cttttttcct	300
attccaaaga	ggatcagact	daactddaag	got at at an	attttcaaac		300
antactor.		gaactggaga	cetytetyea	attttcaaac	ccttggagaa	360
gaacggccag	accgagatet	actatgataa	gtgactaagt	ttgaaacacc	tattcaccct	420
gaaataaqaa	agcgtattgt	Caagecgact	atataataga	tttgatcagc		
taacasaaas	+00044	Judgooguct	gracaatege	LLLgateage	caacgctatc	480
eggecaegga	cacaceetgg	atcatgagtt	gcctgtattt	cgggagtata	acaagaccaa	540
gtgccgatat	tgatcaagcc	ttgtacattc	naanacoata	agttccttgg	- unguocau	
ctcagaaag	+	· · · ·	gaagaccatg	agiteettgg	agaatatttg	600
cccayaaayc	tcaaataatc	aatcttgaaa	g			631
						031

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 879 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

#### (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...879
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310

tacacancag caccacgaag tggcgaaatt teegeatatg cagaaatatt tttegtatat 60 actocgataa attttogtat atacgggaaa taaatttott atatacgcaa atatatttot 120 ctatatacac aataaagaga ggctcggata ttgctctgga actctatagg agaatgaatc 180 cagagcaaag ggctaatctg cttgtgtaaa cctaagggga aataccgatc gacagttgta 240 accccgcata ggactaaccg gtatgtctgt aaacatatat gaatcccgcg cacccaactg 300 tcaacttttt tcagtacaca acagtttgcg agaatatccc tactttacac gtaaagaaaa 360 tagaaagcaa attttgatga ctacgtccct ttcaacaacg atgacctgaa ccaactggaa 420 tctaaaggca tcacaccgga aaagcaatgc gccaggtaga agctctcaga tatggattcc 480 cgtatcccaa atcattgcac ctgcttcatt agagaatgga atcatgcgtt tggatgaagt 540 gacaaatccg cttatctgtt ggaatgggac agatatttga atagtccgac tgcaacgttg 600 tcaagtttgt accggcatcc ggtgctgctt cgcgcatttc aaggatttgt acaacttcct 660 720 tgatgccgat tcaatgagcc aactacgatg cagagaaggc gttctttgca caccttactc gatttgcatt ctatgctccc ttaacgagac atgcctgcgc aatgcttggc gcacagtgcc 780 caaatcatag ctttcaaaga atacaagacc gtggtggaga atctgctcta tccaaaggtc 840 879 ttaactatgg caatcttccg aaaggttgct tctctttca

### (2) INFORMATION FOR SEQ ID NO:311

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 967 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...967
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:311

agccgctgtg acgacgaata ccgcgaaaca caccaaaggt atatctgcct tctgatcgaa 60 tatgtgctat atcgaaacca tccgcatcga agacggccgc cctatctgct tgcgctccat 120 caggaacgaa tgagccgcac gtgcgacaaa agggctttcc cctcccggaa ataccttgcc 180 tgacgaatct atgcccccgg aattgatgtg cggaatgacc aaatgtcgta ttctatatgg 240 taagggggca tttcggacgt ttccttttca ccttatacac cacgccaaat atccccctgc 300 gtategtaae ggeteeagee gatttggaet atcatttgaa geagttgaee gttegtetet 360 cgaagctctt ctcaagcaaa aaggagaagc cgtgaaatta ttatcctgcg caacggactc 420 ctgacagaca catectacae caceteette tacatategg aggagaactt etcacaeege 480 gegteeetet ttagaaggeg tacaaegeeg gtatetgete caateeggte aaataegaeg 540 gcagacetge aaategaaga eetcaaaaaa gcagaagaaa taetgetgte aatgecatge 600 teceettggg geataceatt egtatacace categeaatt attitttgat tateatette 660 720 ggctatcgga tcgagttatc cgacagaggc ttagaagagg taggagatat tgcagatagc 780 cccgatggta tggccgacgt tcgttcggct tgcggatcgg acaggatatg tgagatgaca ceggegtttt gecatagget atacegteet ttetttteat caggtegeea tacacegeag 840 900 ctctgtcatc aggcggtggg tattctgcat cggaatcgag actacagaga ggaacgcacc 960 tocacgoott ototattacg ataggoatag goaaataggo cagogtgata gtogagotgo

tctttct 967

- (2) INFORMATION FOR SEQ ID NO:312
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 547 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...547
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312

ggggtaacga gcgacaatat attccccgtc atcaaaaaat tcctgtacac gaccatgaga 60 tatteetgeg tgagategte tecaatgeeg tggatgeteg cagaagetga aaaegettae 120 atccgtcggc gaattcaaag gcgagacggt gacctccgcg taacggtcag cgtggatgaa 180 gtggcacgca cgatcaggtc agcgaccgcg gcgtagggat gaccgaagag gaggtggaga 240 agtactcaat cagattgett tetecagtge ggaagagttt ettgaaaagt acaagaegae 300 aaggeegeea ttateggeea etteggaete ggattttaet eggttteatg gtgteegage 360 gagtggacgt gatcacgcgc tettteegag aaatgetacg geggtgaaat ggagetgega 420 cggatcgccc gaatacacgc tgaacctgcg gacaaggett gaccgtggca ccgacatcgt 480 gatgcacatc atgaggagaa tagcgagttc ctcaaaaaag aaaagataga ggggctcctg 540 gcaaata 547

- (2) INFORMATION FOR SEQ ID NO:313
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1482 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1482
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313

```
tetegaaaag gacateaett tggatgteag ggeagaggat teaaaaeage gttetataaa
                                                                      120
ttttatagtc gttgaatgag ccgtcagcat gtattcagtc tctatcggaa aatctcttca
                                                                       180
tggtctcgga cccacgatag agagcaaaga agtttatcct cttgactttt tattcctgat
                                                                     . 240
cgtttcctct ctacgctctc aggtgatacc tctggtacga gattgaagat tatgagagga
                                                                       300
atacgaagaa gtgttgaaaa gccggtacga aacacttacg atctaggcgt acgatgctct
                                                                       360
ectgeaeggt geaggagaee ggegtaggeg taggtgeteg ttacaacatg etaattacea
                                                                       420
gtacattatg gccaattaag ggaaatgaaa ataatcttgg aagttttccc tgttttgcgt
                                                                       480
cttcaaaatt atttttcccc cttgtttggg aagatcagga ctcatttctt ataatagaag
                                                                       540
gcacccatga ttgtaatttc caatagtaag agcaacacag actacagaaa ttccccgaag
                                                                       600
agaccggccc cttcggcagg gggctatcgt atttgaangt tgtactccgt atccttggtc
                                                                       660
tetteettet acaattanga tetetacaca ttaattegtg tttatteegg aeggaacate
                                                                       720
atcagaccta tatttaaatg caattgccct gctttggatg tgatttatag ggtatagaaa
                                                                       780
geggaatate ggattttgag acettttgea tgetatagae ageagagtta aaggaatagg
                                                                       840
attcatttat atgatgtaaa aaaggattgg ttttatgatg atttcttgtc ttcggaaaga
                                                                       900
caaaaattca aaaaccaatc cttcttaata ggaaagagtt gtaacggtcg aagtctttct
                                                                       960
cagacttegt tateactgat geettteaga gaggetaeat geececaggt geetecateg
                                                                      1020
agtacgttga gaagccgttg cgttcgagaa tgctcttggc ctggctgctt ctgttgccct
                                                                      1080
gcgacagaag acgatgatgg tcttcttatt cttgagttca ttcaggcaga tgctatccgg
                                                                      1140
tecageggaa tatteaegge teeggetaca etgeetatge aaatteaeee ggegtaegea
                                                                      1200
catcgaccag aaaggcgccg ttgcgatagc ctcactcaga gccttatcgt cagactgcga
                                                                      1260
gaatagattt ttcataatcc taacatgaca attgcgataa tgatggttaa ggaaaacgat
                                                                      1320
                                                                      1380
attttttttt gacactttgc tttgacatac atagtccgtt ttgggaacac cgtctgcgca
                                                                      1440
atgettgega atcegeette gatgteegtg aaattaegat acetngegag agtaggatge
                                                                      1482
tggatgcaat catactgcgg tatncaccta acaatgcaga ta
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 396 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...396
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

-++	aggtatgtct	gcgactataa	gcgactccat	togotootta	tccgcacgat	60
gtgctcggaa	aggeacgeac	gogaotatat	getotgacat	agtaaccgtt	ggacaatgaa	120
ctctccgggt	gtgatcatat	gageactett	t-t-t-	agentiactt	aatatgaagc	180
tgttcgatga	aaagtttgct	cccgggcata	tgtetgeaac	agectegeee	aatatgaagc	240
tgagcgttcg	gacgtagttc	gcatacccga	ttcgtccgaa	aaagaagega	acaggacatc	300
ggatgeteat	ataatctgaa	accaagatct	cgtgtacaat	gattgactig	Lycalyaday	
dacdaaaadcc	caaatcgtct	tgaaagtact	ctgccactcg	ctcaaagata	tgccatgtgg	360
gacgaaagco	tagggatoga	gattgtcaca	ataata			396
aaactcttc	Laguage	gaccgccaca	5 - 5 J			

- (2) INFORMATION FOR SEQ ID NO:315
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 475 base pairs

- (B) TYPE: Leic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...475
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:315

ggcgcagaag	gatatgaaga	atgtgtccac	cggagcggat	gcccttgtag	gcggaaagtg	60
ctggtgacgg	aaaccataga	tccgacgacg	gacaaaggcg	cgtggctgtg	gatggagatg	120
tttggacggc	tegetetetg	acaggggggt	gatagaaaag	ggtatgcgtg	tggaaatcgt	180
atcttacgaa	agcatttcct	gaatgtagtg	gttcttggta	acgacaaaca	ataataatcc	240
aacaaaaaac	ttatttcatt	atgacagcaa	caggatttat	cettgegget	ctgacattct	300
tgtgatagcc	attattgcca	atggcttgaa	gatcgtgcag	cageegagae	catgatcatc	360
gaacgacttg	gcaagtatta	togtacgete	agtcgggagt	caagtatcat	catccccttt	420
			tegettatae			475

- (2) INFORMATION FOR SEQ ID NO:316
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1884 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...1884
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:316

acggatggaa	gccactttga	tgatcaacgg	atggtcgttg	tcgttaatgt	catattgatg	60
ccggaaaggc	gtatcacctc	gtgcaactga	tttgcnacgc	tcattgatga	tgccatagcg	120
gggcataaaa	atgcgcacct	cgntgcccgc	tcctgaatgn	gtctgaggca	atttgcgcga	180
aacgaccgat	atgtcctttc	cggcaagtag	gggaaaattt	cttgggatat	gtaaagaatt	240
tttttgaato	cattctttta	ccgtcatcta	cgtttcttgc	aaaggtacaa	aaaaactcat	300
cggcaagata	aggaagaagt	acgtaaagcc	ctcttagata	agttaaaaag	accaaatacc	360
tcaagaatcg	cactgcaaag	gctaccataa	acagetecca	aaaccagacc	taaacggagg	420
agaccaaagt	gcgaatcgag	aacaaaccac	tcaaggatga	gcacctgatt	atgagaggat	480
	atccgacaag					540
ccaccttttc	acgagccaaa	aaacggcgac	teaceggeee	taaaaatggg	cgcgtaaaag	600

			+2000000000	acqaaaaaaa	tctcqcgtca	660
ttttcctttt	ggtgcgagaa	aagaaaaatt	-tttaggaat	tecagaatta	tecggagate	720
cttttcccaa	aaacacgaac	cgcaatgcag	ttattagtag	tttcatatat	gattttcaca	, 780
ggctgaggtt	cgagaagacg	gttgggcgta	ttattegtat	ctccgcgcac	aatcagagaa	840
		addattaatc	Cacauuccuc	Cogaace		900
	+ 202022003	паасааадат.	uaucyaayay	CCCGGGGGG	, ,,,,	960
	atoccetete	caccdatatd	aaqaqquucuu	cgacogoom	,	1020
	agatgaggag	ataataaat.	Caddadadadad	gaagaagaaa	• •	1080
	aggtttccaa	taaaatcaaa	defeedrere	tycatacyce	33~33~32	1140
1 1 t	++aaaaactac	ccttcgttca	ggcctgtgca	getteegee	00944	1200
	aaddacacat	taggactact	acceaeqqeq	geggeaagag	0	
	agatactact	accaatttaa	CTCTCGLGGL	aacyccaccy	accepter	1260
	antatagget	tacaccaaaa	ggggatcaay	gegacageeg	00000	1320
	aggagattat	CaccacdCLd	gacaactyta	cccacggccg	•••	1380
	aaaaaaaaaat	ctadactcaa	aacttttcc	cyccycccy	~~	1440
	at aat aat aa	acdaatdtca	tatatateee	agegggees	09	1500
ggtaagtety	tctcgataga	degateadd	aggcctgcc	ggatgttccc	gtattggcat	1560
ccggcatacc	tetegataga	gacaccaggg	cgacatacaa	cgcatcctcc	gatttccgag	1620
tgactgctcg	getaeaegge	ctttttaaa	cccaatctqt	catattcatc	cgccggacgg ccgtcgtata	1680
ccgaacgtgc	tgagaaaaag	-tentated	tragnacata	gacggttcgg	ccgtcgtata	1740
cagacaaaga	gacgatgetg		gaacacttct	Caacaaaac	ggettetegg	1800
ctgtcgcaac	cgagataagg	egeggatety	gcacgccco	tacggcaaaa	ggcttctcgg aagctggatg	1860
ccgatttcta	tcagccggtc	teaceatgtg	acacyggaaa		aagctggatg	1884
gaggggaacg	, ccggatcatc	gtet				

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 513 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...513
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:317

				aggagetega.	atcocaaaat	60
aatattttaa	ccacacaagg	tacagttagt	tegeataget	accagetega		120
	astetaeata	accdaadadd	catalccury	Lyggcaccac	009099	
tgtteeeeya	aacacgagee	uccjunjuji	++-0++0000	agcatctgga	cagtatcatt	180
gggcgaaagt	gacagecegg	gggctgatat	Cleatingea	agcatctgga		240
	ateccacat	acqattatat	Eddedracac	acaccacco	000.00	
gccaaggacg	acaccacgac	uoguttu.	aratcata	acacaggata	aactgtggcg	300
ctaaqtqaag	cgtttgctta	cgcctactat	Caageteata	gededajaja		360
	aggetatet	cagtcgccac	cccqaaatyy	acaacycacc	9~9~~555	
Callettega	aagaccacc		agagaattt	ggagaattgg	catecetttt	420
gcaaaacatc	ctactacacc	acggagagtc	Cyacaaaccc	ggagaaccag		480
oott saggag	daadtadaad	cgagcatgta	accattgatt	gaatcatatc	agcaacatta	
CCLLaayyay	gaageggagg					513
tgaatagaag	cagtatctta	tagcattggt	Cac			

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1350 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...1\overline{3}50$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

ccttggctct tgagggtagt tttcactacg gattggccga ggggttagcg agaaggctat 60 cgtggggatg cgttgcgtag tacctttcgg agccaagcat actatacggg gattatcatc 120 ggactgtccg acaaacgtcc caatctgaaa tttcattcaa ggaggttctc ttcctgcctg 180 acgataagec gteagtaett geeteacage tgagtetgtg geagtggetg teggettatt 240 acatagtacg cagggagaag tactccgtgc tgctctgcct gcagcattac taccgagage 300 catacegica tecattataa taeggnaett tgaaageega eageggetta giegigatga agaggagete etegatattt tggagtegge aaaggaegaa eetacaeget tgaegeeetg 360 420 caaaaggetg teggeaaacg acgattegeg ettttaeete ettggtegaa egaggggeea 480 tacggctgga gaagaagtaa aaagccgtta taagcccaag tcagaagtat tcgttcgtcg 540 gcagagcett teeggaegga aaagaetttt geetegette tggatagttg categtgete 600 ccaagcaatc cgcccttttg cttcattggg cagagctata acagagcact ccctcccata 660 tteeteteeg atgeegeaaa ggetaeggeg gagteegate eteatgetae agteaceett 720 tecgetttga aaaagaaggg atttttetat eegaatetgt tacacaeteg gteatgtatt 780 cggcggcgga ggtgagtacc gcttgtggga gcagccccaa gaggaagaaa aagcattcaa 840 teggaagaga gttetacaga eteegeagta teggettete taeteaaaaa eetettete 900 tectetatae geatgaettt egaegeaaag aaaacaaete ttagaatgga eggaagaagt 960 tgtccgttca ggaggccaag cctgtacctc tctccggaag cgaacaaacg aggaggaagc 1020 gatactetge cacacgtatg geogagagge tgggcagttg tttgctatec tateatgett 1080 tgaaagcgat gccaaaaggg tggaagtgtg gaacagattg gccacaagga atatccttgc 1140 gtggtgetgg gtgttegate ggeaetttte etgeeateeg tegettgega ttgattateg 1200 tggacgagga acaggaatac ctctaaaaca gcaggatect gcccccgat tccatacgcg 1260 acaggtggca gctcactcgg ccggatccac gactgccctg ttgtgttggc ttcggccact 1320 cctctgccga ggtgctccac caagtgcgcc 1350

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 402 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...402

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:319

ggagtagtaa	ttcctgaaat	cettgagett	ttgcagaaag	tcgaacaggt	gctcttcaga	60
ttgtccaagg	agaggggatt	gacttacagt	tetteettte	ttttttgtg	agttctttct	120
ttgtccaagg	tttatttaaa	gaagattact	ttcgaagagt	ttcttqccqt	atgeggetee	180
tettggagga		gaagataaa	cttctcagcc	gagettteet	ctccagatcg	240
ttccaaaaag	gagaaageee	caggaccaaa	agagtatato	ctcatcgttg	gttaatcggc	300
ttgtcaggtt	ttteeattgg	tataastata	agageacata	ataaggggtt	ataaccatac	360
cttgctgtag	gegagergee	Lycogacycy	ggcgagggca	ta	gtgaccgtgc	402
cagattgaag	aaagctgccc	agaaatgttt	guococagog	~ <del>9</del>		

### (2) INFORMATION FOR SEQ ID NO:320

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 517 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...517
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320

gaggatcccc	aaatttta	tocaaaaatc	agcccgaaaa	tttgttgtga	acgtaaaagc	60
ggataacttt	gggccccccg	aaggtttatg	acagatatca	teegeeete	cttctcatag	120
atacctctac	ggcacagaaa 	tanatagaat	tactactaca	ggtactatta	tctcacaacg	180
atacetetae	tegegittige	ccaycyyyyc	ancetogoa	tattogtaca	agaggtettg	240
ggttagccat	graggearre	geatgetget	aacaccggcg	tctaagttcc	ggtccggatc	300
acagagcaat	aggettagga	gtgaageett	beengeage	atagettag	actoggaata	360
atataccgga	ctacgcatcg	gategteeat	tgecaaayyy	tracaracas	atatathaac	420
cegettgngt	ctgtccctac	tttggagttg	atgctgaggc	cycacyacca	cogcochado	480
ctgatgggtt	gatttgccct	agatcgacgc	cagacgtatg	gaagtttata	Cagcacccc	517
cgattccaan	gtaaagccct	tactgataca	ctgctct			317

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1385 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN



- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1385
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:321

gcccaggctg	aaaccgaggc	gaaaatcata	tttgctcttg	atgggcattt	ccaccaaata	60
gaacttttga	gtccgatccc	cggtgaaaag	ccattgctac	tgtggcaaca	tcttcggact	120
gaagtacaag	gtcactgcca	gctcttggta	ggtgtcatag	tggaccttgc	tcttgggtat	180
cggtgagaaa	agaatagggc	gtcattgggt	ccatccccaa	tacgctccca	gatgcttggt	240
ataggtatcc	ccaaactgat	gaggaagcgg	ccgagagctt	ttttgtcaaa	aaagcttctg	300
cgtcttcgaa	gactattacc	ttttcaacaa	taccaatgat	actgggacat	tcgtatacat	360
gagettegga	cttccggcct	cttcccagtg	tgtcttcttt	catgtattcc	taccgaaaaa	420
tccaaccctt	cgggcagaat	gtgtggtgta	ccctcatccg	tatgctcatg	tccatgccga	480
agatattgcc	ccaaaaccat	tteeggeegt	ggccgaactg	aaagtggtag	ctgcctcaag	540
ctcttgatct	ttaacttcga	ttgggcattg	gccgagagac	ccaaaaacgg	agtaaagcac	600
atatcgatcc	tgtcaaagta	gtttttttca	tttcagtatt	ttttttgtgt	tatcgattct	660
aaatgggagc	gaaggtatca	aattataaat	gattgacgga	gccggatttg	gaggaaaaca	720
ttttttctt	gcagtttctc	tttttctcgg	gcgtgttttc	tggattgtac	gaaagaatac	780
ctactttgcc	ctcgacagac	cgctacgggg	gtgcttgccg	gcaagaattg	cgaacggcag	840
gctgagataa	tacccataga	cctgatccgg	ataataccgg	cgagggatgt	agaatcgaat	900
acacactatg	cgtgccagca	gcttcgggag	agcaccccat	tgtggacggt	caaccacatg	960
tgaaagaaca	gatattatcc	tcaaaagcac	gcaaatgcaa	gttactatca	acaaccaacc	1020
gatcacatgc	tcgaaggtat	gggactggct	gccctcttgg	aagccgagcg	gatccaaggg	1080
agcgcacggc	catagccgta	aacggagaag	togtaccccg	tgcctcgggc	cggacttccg	1140
tctgtccgaa	ggcgatgaga	tcctgatcat	ccaagcacct	atgggggctg	accgacgtac	1200
cttcagcttc	aaggcgatag	tctcaaacag	taaaaaccca	aacccattac	ccgattgata	1260
tgaaagaatt	caaatgacta	ccggtcctct	gccgggcagt	gagaaaatct	atgtcgaaga	1320
gaacgtttcc	cttctggcgc	gtaccgatgc	ggcgcatccg	aatgtccgac	acatattgga	1380
gaacg						1385

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 527 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...527
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322

gagategtte agattg	cctg tccccaagta	tttacgggtg	tactggacgt	geeteettee	60
acttgatcaa cggatc					120
tagcaatgga tttgga	aata ggaaaaacat (	ggcgaaatac	tcaatgtttc	ccattttcct	180
attqtccttt ttcccq	tete ggeataceae	gtaattccgg	tagatgcacc	gaaatcgaag	240

		atactcccat	adaatuccca	Clatageege	acgttgtgcc ccgttctccg	
agacggccaa	~~~~~~~~~	agtgtaaggc acccaatgat	cagggcatac	caccgaageg	tgagcctgta acgcatacaa	, 420 480 527

- (2) INFORMATION FOR SEQ ID NO:323
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 474 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...474
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323

togttcatct totcagaaga aggaatatgg atatgccaat atottatata tggttacttt 60 gctaatagat aatcagttgg gggcgattat tcgtaagtcc agaattttga agaactttct 120 gatttgatta gtaaacaagg attaattctc gaaaattagc atctttcgga ccatatttca 180 taaatgctat ggtaatctca agcaaagtaa ggttatcgct atatcaggcg atgttgtgca 240 attaatgatt attetttee tgatgagaat ttgegtteta agegattgga gagattatea 300 atgataccaa tgttttattg gatatgtgta gtaacttatc ttcaaagaaa tttataacaa 360 attgaatgta caattatgaa totatatatt goagoataaa agttgtggtt caaggggttt 420 474 aaagaaaata cagaaagatt cataacctac tcgttcgaac caaataaaat taat

- (2) INFORMATION FOR SEQ ID NO:324
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 395 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...395
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324

ggcttcaatc	cagcatcttc	gatagcgttt	gtcataacca	gcttggctcc	aacccgtcag	60
gatgacttgc	cgtcaggtga	tatgcatcgg	ctgaaagact	gttcccacca	attcggcata	120
gatgcgagca	ccgcgtttaa	gagcatgtcc	agttcttcga	gaactataca	tgctgctcct	180
tcacccatta	caaaccgtca	cgactggcac	tgaaggggcg	gctggcctct	tgtggagcat	240
cgttggagtg	gagagagcat	tcattgcatt	gaaacctccc	actccggcag	cgcaatcgac	300
gcctcagagc	ctcctgcaat	gattacattg	gctttgccta	agcgatcaga	tggcaagcat	360
cgatcagagc	attggtagag	gaagcgcatg	cgatg		-	395

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 614 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...614
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325

```
ggaaagaaag caagagaaac gaaaaagaca acgaagcagg atcgacggtg ccgacctctc
                                                                        60
ttgaagaggg taaccaacga tacagaggtg taacctttcg agcactatcc gtcaaagagg
                                                                       120
caaacaaacc caagtaataa ccctcaacta aaaagaaacg attatgaact tagaatctgt
                                                                       180
tttggtacct gcggtatgtt ctacttcatc tttaaagatt ttcgaactct acgtacgccg
                                                                       240
aggegaegae ttegeetgat egagaagete gaeteettge etteteeega aagaatgeag
                                                                       300
acttaacaca gttaacttcc tcctttagca cccgagacaa tcagggctcg gcatcaaagt
                                                                       360
aggtttcatg atggtaggca tgggcatcgg acgntngctg gctttctttc tgacatttgt
                                                                       420
tttccaacgt gtaatagaaa acttgacggc tggagcttcg gccacacatt cgaaaccctt
                                                                       480
togggaatet tetgetgatt tttggeggte teggaettet gatteettee ateateatgg
                                                                       540
caaggagaag agagacaaac aataaaagaa caatcgcaat aaaaatgacg acatcaaagg
                                                                       600
catccacaaa actt
                                                                       614
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1023 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

#### (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1023
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

ggttttaccg tggtctacgt gggcaatgat ggcaatgttc ctnatgtcng cattttcttc 60 ttctgagtaa ttggggacaa aggtagtaaa acgggctgtt ttcggaatgg atatccaagt 120 gttcggattc tgcacattcc atctgcagag cgttgcattt gcaggcaaaa aaagacgccg 180 acgaaagtgc tctcatggcg tcaataggat tccaagatat ctcttgatag agtttttcag 240 ctgacatate egtettaeag gatgatgtte ttagatgtet gtgtattate ageaacaaaa 300 cagtgacgag aatatggcct ttcgtcttta agtcgataca aaatctctgc cctgtgtctg 360 actcgtggca aaaagcatcc gtcctgccat atataaatat agaccgattt gatcagtttt 420 tetgeettga tgeegatggt etteettgga tgtagaegtt tatategtte gaegaaggta 480 caactgtttg ctatctgtcg tatggcatga tttggcaacc gtgctataga agataatgga 540 tactteaget gataateetg cacaatgtet eeetetaeee tgaegegett tggaggggat 600 660 aggagtttcc ggctatcatt acttctccgt tttcactctg ataaagttgc cttcgtcatc tttgattgcg atctcgaagc cgctgtgtct tttacgcaaa caatagtcgc tgtcacttcc 720 780 ggatacgtaa attgcgcata gggatctcgg taaccactcc ctcgaaagtt cgattgggga gagtatgcgt gtgcacatca gttcatagta ggcatcgaat tcatggaaac gacttctgta 840 attagcatat cgcccaactt ggcgtatgga cagaactccc ttacccccca taataagctg 900 taggataata ataacctttt ccctgataac taatggtgct ctaaaggcta tcggttgtca 960 aaggcattca gttgtgcatc cagaccatcc ccagccgagt gataatcgac cgggactgtg 1020 1023 tcg

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 444 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...444
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

aggagetttc	ctccttcacq	atttcatcaa	tatccaatgc	ttcgataaac	ttgcaatgga	60
ttaggetate	accutctcat	tegtacgegt	cagageetea	acgtttcgta	tggattggga	120
tecogciac	tacqaaqaat	agtttgttag	cctcagccac	cacagcatag	ttgttctgca	180
eatcoccatc	dadagggtt	cattaagaag	cagtttgcca	agccctttgg	ctatgctcgt	240
aaccccgacc	gagagogoco	caaaggagtt	ccacattaca	aagtacagtg	gaatcgtcag	300
etataataa	aagggggaaa	taggcaattt	gcgcgacaaa	tgccaaatat	ggcattcgca	360
attacage	tacetteaac	attttcatag	gtgatcggat	tcactttatg	tggcatggca	420
	cctcgccgcc		90940099	•		444
yaayaaccya	cccgccgcc	cyac				

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 711 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...711
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328

aagcacttac	addacdatac	atacet				
	555acgacac	acayytgcac	gccggtcgga	cgaattgcgc	tgatgatcca	60
regeetttt	cgcatcggga	caatcatctc	cctcatagea	cetteetet	tetgetgtte	
ccaaccactt	tactttcaat	~o+~-~-	Journal	coccyclota	leigetgtte	120
**	egeceegge	yergagtaca	aatacgaagt	gatagagcat	getegeegtt	180
ttgctttctg	ggcagggtgg	taccgatcgt	etectttacc	actttcctat	gggatggagt	
attegggggg	CCactggate	2022		geeeeeege	gggacggagt	240
	couctycate	aaaagccatg	cggagagcca	tgacagetge	tttcttattt	300
Lettegeeae	tttcttcctc	cttcqtqqaq	ccttgggcga	gacgcccttt	aaataaaa	
cgtcctctac	ctcctcacac	aceacatast	~~~	,	ggctegeett	360
~~~~~~	- to to do go	geageetgat	gcgacagtat	ggtaccgcag	gcatttttc	420
ju-guace	geeegeaaag	yyctgacacc	ggaattggtt	tatacataac	tttcccccsst	400
caagcaggag	agagagaatc	agatactord	2500000		cccccgaac	480
actttagggg	22222	agacactegg	ateggeageg	gctctttcgg	ttgcataccc	540
	uuuucaacaa	CLLTGCCacc	agtgtgaaat	CCAAAAACAA	taassass	600
gaaacgaata	aatcttctcg	cagetteaat	gaagetgott	ntntn	oocaaccaac	000
actatoacco	taatata	- Myoucauc	gaagetgett	atatagcaat	agcggccacg	660
30 ca ccaccc	cyclyleege	ctatgcctga	caaaggaaaa	tccqqatcaa	a	711
			- -	-	•	, , , ,

- (2) INFORMATION FOR SEQ ID NO:329
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 507 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...507
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329

gacqaqqqat	GAGCCGAAAA	acastassta			tacaaaaaac	
0+0+	·	acaacyaace	caacaacagt	gactcagcat	tacaaaaaac	60
acaccagget	gtcggggatg	gactgctgag	Casaacatca	gostagtaga	+ . .	
ccctcacaac	Aatgganttt		- 3 - 3 3 5 3 5 5 5	geetegteeg	tgcatcggta	120
	au cogcattt	CCCCacagea	tegaegatet	ddadaacata	tataaaaa-	100
tettgteata	cttcgccaag	atatassass	CCSSSSSSS			100
	3 3	Jogogaaaga	cyaaaaacay	geegagatge	tcctctacct	240

naagccaaac t	ctacgatcgc	cttcgtctac	cgctcgcagc	atcgtttcga	aagcettgte	300 360
accttgctgg at teatattega at gnatgeegge a	agcaggctga tagcttgtgg	gacaagcact agggcgatgc	gtcgnaagca	gttcgacgaa	ttggtacggc	. 420 480 507

- (2) INFORMATION FOR SEQ ID NO:330
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 553 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...553
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330

aactactatt	ctgccagcac	ttcgtcgagt	gtctgataca	gcctttggta	aagagcagcg	60
ggccgccgcc	assaggetta	agagegaate	cgatttgcat	aagcctctaa	aagaaatttc	120
caaagteety	caaggcaccc	agagegaace	anattantta	ctacccataa	agggattccc	180
gcccgtacgc	tegaatetge	gataggtggc	aaccccaccc	cogocogoaa	tacatacata	240
tcttgtgtca	gattcactcc	aaccgtcggg	cctttactcg	ggaagcaacc	Lycatayeta	
cadacacada	ttgcagtcta	taagtgtcaa	aatattatcc	atacatatca	aaaaatetet	300
+++++++++	stattatcac	tttcgaagat	aataaaaccq	ttcaaaaaca	caatcaaatg	360
Llattatatt	acyceaccac	agaatctgtt	+++aa+++a+	cataagagat	tatecagtae	420
gactgaacca	ccaaacgact	agaatetget	CCLaacccac		agaagataa	480
tttttcaagg	gtgacatact	taaacgatag	cccgaagaga	tgatttttt	ggccgatacc	
ctacttectt	cagtagaatg	gaagcccqct	cgccgaatac	gcgacaaata	acccatttgg	540
		, , ,	-			553
tatggaggga	aay					

- (2) INFORMATION FOR SEQ ID NO:331
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331

ccactattgt tgcgtatgat catcaatttg ggagggtact ctgctatttg aacttttta 60 gttctatggc tacggggagt tccaccattt ttttgtcctt ggtctatgcc cctccactca 120 ggatagtegg agteggaata taettgette tgtattgeeg gatgteggea gaagacataa 180 gcccgaaaaa aagtgcacga acaagcccac gtgattcatc acgaaagcac cgtcacgaag 240 gttcatttca gacgcataag cctgtctgta gtaacgcagc ccagtacaaa gagcaataca 300 gatacagcag caggaagtac catgccgata gcatggagct aagcccaaac gatgaatagg 360 atgctgcaat cctctcccca tttctgcggg gattgtttgg tcagccccat gatgactgca 420 agcagcagta gcccaccgat aaagtcagag tggctatgtg gccagataga aaggagaaac 480 gggccgaatt cggcgtatag ctctacgatg gaatatgccc caaaacaaga tgccggcaaa 540 agcaaacttc ctccgaccag attgaaagga tacagcgaaa gctgtggcag tatcgggcct 600 gcgatcacct ggagcaacaa acctacaaaa gcaagtctga tatgatgaat atgccttccc 660 tatagccgaa gcgtccctgc cacatatgtt gtatgccgaa aaaatagtaa acagtcttag 720 tgaaaagaac agatcgtctt atcgtattag accttatttg gctgctatca aaagaccttt 780 teetttgett tetteaccea ettgggcace actgteteca agaactttte tttttettgt 840 gcaacccatc catatccaag cctatatact tctgggcttt ttttttggtgg agacatcagg 900 cagtggtacc tcatccgtat agccatgacg tcaagtaccc gagctatctc tatacgtgct 960 tgcatcgcac gctccagccc ttgctgagaa tacgtgtaat ctcttgcggt gcatggaatg 1020 aageteeata gaageeaete eatagteeea aegeeaetgt gattggegga tataettagt 1080 atgggggtca ttttcctttt ct 1102

(2) INFORMATION FOR SEQ ID NO:332

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 592 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...592
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332

```
gcacatttcc gctgaagcta agattgttag ttgcataata ggaaagcgat ggcttacacc
                                                                        60
ctgattttcc tgtgcacgaa aagttttctt atacgtttct ccaagaccgg ttcgccggat
                                                                       120
cettttttet tttttattte gaacggatat tetgecagee atcegtatgg tagaagaaat
                                                                       180
agttggtatt gctactaact taccgatgtt tatatcgagc gaagtattgg tttgccgatc
                                                                       240
gttgtcttcg atatgcgatg tgacgtatat gcactcagtc gattcgtatt ctttttgtga
                                                                       300
tcacattgat taccccggcg atggcatcgg atccgtagag cgactcgaag cacctttcac
                                                                       360
cagttcgatc cgttcgatct gatcaggaga aaacgactca aatcggcctg accgcctaca
                                                                       420
togoogtaca caogottaco aogataagga tgaggatata ottactgota aggoogntoa
                                                                       480
getgeatgaa gageeeatea gattggggee gaagteaaaa gaeggaetea geeetgeata
                                                                       540
ggcctcggaa gtaggagccg agaaagaggc tatgtcctta gcggtaagac tt
                                                                       592
```

(2) INFORMATION FOR SEQ ID NO:333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...582
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

cgcctttcag tt	ttcggcagg	aatgattccc	agtcgtcctg	caagtcgcca	atccccatgt	60
ggaagageeg ag						120
tccattacat ta						180
tegtteeggt ag						240
ttggttgacc to						300
aaaagaatag gt						360
aggeegtgeg ga						420
tcccgtgcat as						480
agaggccgag aa	aaccggcgc	ggttaagagc	tacagcatcc	tcgatactgg	ccggccagca	540
taccacgggt at						582

- (2) INFORMATION FOR SEQ ID NO:334
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...476
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334

gaggatactg	gatagtatcc	attgacatac	ttatctcctc	gccattccac	aatctccaaa	60
aaggagaagt	accccccgt	acccggcata	ccatctttct	gatattggaa	tgcattacaa	120
cccattcttc	gaatcggtct	ccgtagtttt	atacttcgtt	ctttgtttga	agtactgcaa	180
tgcttctttg	agttcgcaat	aagccggttc	aatatctcca	tagtatattc	aagaaaatgc	240
gatgtataga	atgtgttgca	tatttattcg	ttgcctctgt	ctgaataact	tctgctctta	300
gctgatttcg	atcggaattt	gaaatgcaat	taagcaattc	ttttttgtg	taagtttta	360
attttatgtg	tgctgttatt	atggttctga	ttggctattc	taatacattc	ttctcgtgat	420

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...525
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335

ggctacgggt	atttttgccg	agatggatca	tettegtace	cgtatctgct	gctggaaatt	60
attggtaaca	gcaacggagt	aaaactccgc	tatogaatgt	Caccacacaa	gacacagetg	120
ggatatttcc	atgtgatggc	agaaccttct	cgacctgcgt	ccaagatatt	tttgaattgt	180
cgcctttgca	gacacccgct	tggtcacgaa	attatagata	ccacctttac	cctctttgtc	
tccggatacc	aattctgtac	cgtagaatac	ttgacttccg	Cattagtata	ggcatgatct	240
ccacgattgc	agcatgaagt	tgattttcat	cccactagaa	Bacatacaca	cttcaagata	300
gctcacataa	qaatcctcat	Cadcaacdat	cacattaatt	agegracage	tgtattggct	360
gcattgattc	ggaaataagt	aaaaactcca	taggeceget	egaactgtee	tgtattggct	420
Caaaggagcc	tcactaaata	Caaaaaaatt	gagagetgea	gacgeetttg	gggatataca	480
33-3	5 - 5 - 5 - 6 - 6 - 6	-yycayaycc	yayayetgea	aagaa		525

- (2) INFORMATION FOR SEQ ID NO:336
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...648
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:336

ggccgttaca ttcagagttg cgtgcatcgg attgccggca aaattcacat actgccttct 60 ttgatgctga aacgtttttg gacaatctgc cggaggttaa attataagtg cccgacaaca 120

gttccagccc	tccqaataca	ttcagatccc	caatgtatgg	taatcgatac	gcaaatctcc	180
accogctgat	ccqcqtagcc	ategeeggte	tgcggatcca	gtatcaaatc	cacctctgca	240
teegggteac	gcctacattc	atgaccaagt	ggaaatccgt	ctccggatct	cctccgtagc	. 300
aggtagaagt	agagaaggac	gatccggcga	agtttcttgt	ctcctcgctc	acggctgctt	360
ttcggatcta	cgaatcgcaa	gaaacgatac	teteegetgt	cgtaggctgc	gtaaagttca	420
					ctccgggcac	480
					gttgtcccgt	540
					ctttgatgtc	600
		tatgtgcatt				648

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 719 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...719
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:337

60 agogtoagot tttoottgaa aggaatgtto ttgooggtgo ggatattgoa atggoggota tgatctcccg tgtacggtcg aaggettgca ggaagteetg teegteteat gegeateggg 120 180 caggaggcag agcatgatgg totogcotog tgacgcggtt cgagtgcatg ccatagctct 240 tctgtgataa aaggcagaag ggatggagca aacgcagcag ctgatcgaag aatccgatcg tactgcgtag gtcttcgcat ccatcggctg accgtatgcc ggcttcacca tctcagatac 300 caggaggaga agtcgtccca gaacagcttg taaaccagtg tcatgcctcg ctcagacggt 360 acttggagaa gagatcgtcc aactccgtct tccctcatcg agacgatacc cgaaccattt 420 480 cacggccaga gccgaggctt cggctgcgtg gacgtttctg cctgctgcca tccttttacg aggeggaagg attecatate ttattgeaga agttaegtee etgeteegag agegattege 540 600 gaagagcaca tegttgeegg eeggagegge cateateagt eccatgegae teegteggea 660 ccgtatttct ccatcagcat gatcggatcc ggtgagtgcc gaggctcttg gacatctttc taccctgacc atcgcgcacg ataccgtcag atatacgttg tcgaagggtt tcttgccac 719

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...522
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338

actcaatcaa	aaagagggta	atcgagttct	tttacatcat	tgaaattcac	ttttcaaata	60
aatatctaag	aggagcctta	tcggtcaatg	agatacctta	cattgaccta	aacaacacct	120
attgagagat	gctatttgct	tgaagccata	ctgttttgta	gctccacaaa	gcgattataa	180
gagacaagat	gtggaacttg	ggccgacctg	agcaggtgat	atattgaaga	taaaaagctt	240
tccaatttgg	cgttttgaga	gatgaaacag	gatcaggatg	gtcatgatct	tgcttccgag	300
atcttaacct	ttctattcca	acgtcgaaca	gacattgtaa	ttatcacaaa	ccggaccttt	360
ccgagtgccg	actctcttc	agtacacgtc	atggcacaaa	agaaacagtt	gttggactca	420
acttacaaaa	gaaacttttt	caaaacactc	ttctacggaa	atatcgtata	tatttgtatt	480
caaatacata	acccgatgaa	acgcctcctg	ctctgcctca	tt		522

- (2) INFORMATION FOR SEQ ID NO:339
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 566 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...566
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

cggccatcga	aatcatactt	gaagataagg	ccaaggcctt	gcgtcgtcag	gactggcgca	60
gatattgata	gaggttgtta	tagtggttgt	aggctttata	cgaatggagc	cggacggatt	120
gattttatat	tcggcatcaa	attcgccaca	taggtattct	gtagattagg	attgtcccga	180
tagcccacat	tcccgtgata	aggagacngn	tattcagcaa	acgactactc	aggagcagtt	240
ctatacggtg	tcctgaaaag	aggtgttggt	cgtcttgatg	ctcgttccta	tctgactttg	300
tcactaaggc	ttccgagcat	attggtgagc	tgctgcgaca	gagggtggtg	gccactgccg	360
tccagttgtc	tgtaccgctt	cccgaattat	agcattctcc	ggcgtataaa	actttcctaa	420
gacaagaaga	taaacgatct	gttcgtcatc	gaatcttcgc	tgtggatgag	actgcgaacc	480
cgacgctcca	ttcgctgtcg	gagttgggta	gcttgatgtc	gaaactgaca	gcaggcttga	540
acatggcacc	attgatctga	agcagg				566

- (2) INFORMATION FOR SEQ ID NO:340
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 557 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...557
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340

cgaaggctac gtcatctaag ggcttaaccc gagttggaac atggtctggc	gagaattgac gatcttgccg gccttgtgtc ttttcgtatg ttctgcacag cttcgatggt	atacttggcg cttacggctg ttcgtatcgg gcttcgtcgc tctccggacg attgagaagg catcgctctt	gccttgtctt tacggggaaa atggaaagcc tgaaagccga aatacctctt tttttttgaa gagtttcttc	atgactogcc ctgtgtcgac cctcttttca tggggaagta gaagtcattg tcctcatcgg	cgcggaaacg taagtattcg ggagatagcc tgtcatccca gcaaactcat tcagctcccg	60 120 180 240 300 360 420 480 540
tgagaatgaa ntcgtgaatc gtctatttca	tgatncccga	categetett	gagtttcttc aaatagcgca	aggetteget	atagetgagt	

- (2) INFORMATION FOR SEQ ID NO:341
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...522
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341

++ ++ o++	taacetetae	atactacqqa	catccatctc	gccatctgat	ctggtcggtg	60
ttagettett	annaganna	accaccataa	ccactctata	tatcgactat	tccgaaaaat	120
taaceggtac	gaacggcaag	tanatacatt	tgcaactatg	tggatgaccg	gtccgaaccg	180
gggatataaa	geeggtetgg	coattaggat	tgaatgetet	tttccgtcga	atggcagatg	240
accactcaca	ccacacggac	tageagttea	ctctcatgca	gcggcacaaa	agagatcggt	300
caggtgcgaa	tatgetttta	astatttaaa	aatcttactc	gtgccatctt	gactatcacg	360
gctcttgact	tegateggegg	aaccccacg	aggtttttc	gatggcctcg	gtgcttcagc	420
gctccgtacc	ggagtattig	cgagecaaaa	aggeteetaa	taatacaaaa	cacccgagea	480
tttcgcattg	gtcaatgccc	agacaagaac	ggeetegeaa	tggtacaaaa		522
cgtgtatgta	ctatgcactg	agageacyge	aaactatcga	90		

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...409
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342

ttcgccctta tattcgatgt tttctcctgc acggtgataa	, , , , , , , , , , , , , , , , , , ,	gatgttcgtg acacccttgg attgatttgg	tgatacaggg tttgagcttc tctgtgaggg	tgttggcact tatccctaag aataacggtt agacttattc		60 120 180 240 300 360 409
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- (2) INFORMATION FOR SEQ ID NO:343
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 589 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...589
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:343

cgtctgtccg atc gccacggaga tgg ctcaagcata ttt ggaatttgcc agai	gtgtgat cgaatatcaa tgacaac aatctggagg agcggta cgcgtaatgg gcttacg gccgacggtg gtcaatt tcctgaatgt cggcaa ggctttccgg	acagaggtgc ccatgaaggt gcagaagacg	attatecteg gecagtteaa atatettegt ggacgaatga	actgcgagat cctgatgttt cccgaaacgg agatcctttc	60 120 180 240 300 360
ggatgcgcga atto	gaacaa atggagatgc	agtettegta	cgaccgggtg	aagagetgea	360 420

gacaaatacc	tttccatgat	catgccnagc	cagtggcacc tggcacacta agtggaaggc	Egocaacycc	cttcggagac gccaccgatt	480 540 589
tgagttcgag	atgeegiteg	gccccaaaga	uguggaagg-			

- (2) INFORMATION FOR SEQ ID NO:344
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 726 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...726
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344

aggtategge geegatggta gtaceggagg egatecttga egttecteta geaegtttte gttgatettg	ageceegage gtggtettge gtaggtgaag eggaggatag taegtttgat caattegtee gegaataegt gaataateeg	acgacgetet etacgeettt etgtegeeat tegteagete gatetteaat aagaceteat ttetttggte aataateea etcataateg	acgcccacta cggccgatcc ggaggtggaa gtggtatcga cgccactttg ttggacaggc tatcgtatat aaccggcgca	ctcttaccgg cttcgtccaa actgttatat acacctcttc	ataaggtttg agcagcgagg cgcggccact gaagtcacca ctacggcacg agtctctttt ctcttccttg ttcccgtcgg	60 120 180 240 300 360 420 480 540 600
ttctttttcg	gaataatccg tcttgtaatc	aataatccca ctcataatcg	aaccggcgca caccgttaac	acacctcttc atgtcgtctt	Ccccccc	600

- (2) INFORMATION FOR SEQ ID NO:345
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 693 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

tctgtacgac gccgaatggg gcggcgtcct ttcgtttctc caggccatcg ccgtctatgc gcgctcgtcc	gaacgcaggc ttcatcgtgg gagccgactg cggcctgggc gtctggttcg gcgacggtgt gcgtcctctc gaattatcgg	gcaccatga gcaccatggc gccgagaagt tatatcatcg ttatcatgcc gtcgctgact gcatcggagg ccggccgtca	agctgctgtg tggtggacgg acaagctggt gtctgcctta ccttatcggc atggcctgat tatcgccatg agctggccgg	gccagcggac agaacgtttc ctttaaggtc tgccacgatc tactcgcccc gagccctgag gcgggtatca taccgaattg	cggtatgact gatattttcg tcgggatcct accggcaagg	60 120 180 240 300 360 420 480 540
gegelegtee	ategatgage tegetttgtg	ccggccgtca ctcgcacaca gtgacgatgc	agctggccgg gcgtgatctc ttttcttagt	taccgaattg tcnatgaatt	accggcaagg cattacgcnt	

(2) INFORMATION FOR SEQ ID NO:346

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 839 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...839
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346

ataccgccgg ggaagtgctg cggttagacc aggctatgcc	cattgeegg caaagcgttg acgcgcatgc cgtatataat gaacaaatgc	gtagagetta caagetggat teggagggea ttegetacag	gaggtgcacg tgccgtccac attgctccgt ggcttacgga tgcagaatat	catcaagagc gtggatccgc ataagggatt tgcaacgata agctcctgcc	tacagacagt	60 120 180 240 300 360
tateggeeag acatetgete gaegegatgt	aggaggcacg tatgcgtgag gactggctcg aagggagacg	aagattgege aaggacteea caeggeegae aagataeteg	tccacctccg ctacggcatc gcttccgctc ccacgatgat	acgggcgatg aactttggag cactggccga ttttccggcg	gacggtgtac tcactcgcga ctatctgtga aagaactgac	420 480 540 600
gcaaagagac	tactttgaca	tgatgaccgg	ggccgacacg cgatccggag agtatggacg ggcagaagaa	catcggccga cttgcaagcc	tggatcgaga agaatggtta	660 720 780 839

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1903 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1903
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347

atggtattet teegetgtae aacegttgga ggggetteet ateaatageg ateeggateg 60 120 gagategege ggecaegatt ggeatgetga gegtagegaa attgateatt getgeateee 180 aaataccatt gtcgcgttta gaatatcacc agctttccac ttgtcttgaa tgtcgaaaga 240 ggtacgccaa ctgccgcacg caccgtatgc cccaagacca gggcatcaat tcaccccatt 300 cgcatcggag aagaacggag gacgtcccgt tgccgcaagt gcgcgcccca tggcccatac cgttgctgcg caacgatgga tataggcggt gaacagcagt agtgtatttg ataaaatcca 360 420 caccccactc ggagaatgtg geggeateta tecetette teaaaactae cactcaagee 480 atgaacgtta agaggagatg cttggaggaa aggccgagcc gcataccgcg acgatgcagt 540 tcatcggcca atgtttgatc ccattgggga aacgtaaagg atccgcctta attctcccgc 600 gctatcacgt acggacgttt gccagtggct ttctatgatg atatggttta tccggctgca accagteett taetttgeat egeateggee acateeaaat agtetgeteg tttatttett 660 teteetteag ceaacgtgta etecaaceat aacgggagee aatecattat accgaeteae 720 ttccacctgc caaatcaact gtcggcaccc gattcgttgg ctgctgatat ttcaaattcg 780 840 aatagatgcg agaagaagcc ttaccgcgaa taattccttc gtgggaatcg aattaaatcc 900 ttcgggcaaa tgcttgatag cccaatgcgt ggggcgtgat ccagataagg tatcttgaag 960 gtocattoac gatocatggg coaaatagat ctoogggcaa aagaatacgo ggactacoot 1020 ctgtcggact cagtgcatag gagcaggaaa tgcgagaagg agaatcagaa gaaagcctgt cggtcttcca acagagagaa agcgcacctt ttcatcagca gtgtactatg gccaatcccc 1080 ctgagaggtt teettatata gaeteggeaa ateettgeee gtetgaeeat caetteeaeg 1140 acctgatcga acgaaatgcg gtgtctgcca tcgctgaatt ggcataagta ttggcatcca 1200 aagctcgtgc tgccgcaaag gcattcgttc gatacaaggt acctgcacca atccgcatac 1260 agggtcgcag gtcatccgag gtgatgctcc aaagccatct ctgcagcata ttcgatttgg 1320 gacgggtacc cccgaatagc tggcttgctg gcttgccgct cccatggcac aaccactccc 1380 1440 acttcgccct gacagccgac ttctgcaccc gaaatagaag cttggtgcgt accacattag caaaaaggcc ggccgtagcc agtgcacgca tatgcgctta tcgctgaagt cacgagtctg 1500 ttggaggtgg tggagtaccc cggtacaacg ccgcacgacc cacatgtcgg cgccgttacg 1560 1620 atcttgcccc cgatgcattc tgttcgctca cagccaaagc ataggcatat acattgctcg gettegtaca eceggegaat acceetgege acgaateaga tagetgetge etteeggega 1680 acgeceagte cacceggeag caccecetea geateageee etectgaatg gegeteegea 1740 ttaccgacca gacctcagcc aaatgtccca tatatcggga tcttcgtttt cttccacata 1800 ctcccaatag cttggccgcg cctgttcagt tcgtcgagaa tatctgccat cttgctgagc 1860 1903 ggtatacete gegacetege tgttegttga agtgttegtt gge

- (2) INFORMATION FOR SEQ ID NO:348
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 578 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...578
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348

gggctgcaaa	aaaggctgtg	ctcctcatac	gagatcgcac	tgtcgcccgc	ttgaaagaga	60
caatcgccca	actggacgaa	tacttctctc	acaagagaag	actttcgaca	tececetget	120
tatggcagga	acggagtttc	agcaaacgta	tggggcgagc	tgctgaatat	cccctacggc	180
accacgatct	catacgcact	cttgcacgac	gaataggaaa	ccccaaagcc	gtgagggccg	240
tagccgtgcc	aacggagcca	atcccatatc	catcctcgtg	ccgtgccatc	gggtattgga	300
agcgacaata	cgctgacagg	ttacggtggg	ggattggaca	aaaggaattc	ctgcttcgtc	360
atgaaatgag	tctgccggtc	taaagccttg	aagcctctcg	aaggctattt	atatttgagt	420
atatttgcaa	gcataaaacc	attatataaa	aacaaagtag	aatatggatt	tcatctttct	480
tcaggccgac	acaagccgga	ggcctgttcg	gaggctcaag	ccagatgatt	ctggtgctct	540
gctcatggta	gtaatctttt	acttcttcat	gatcaggc			578

- (2) INFORMATION FOR SEQ ID NO:349
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1530
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:349

gccggtattg	ggcattggtg	atctccggtc	cgatccatcc	aaaaaggcac	caccagatat	60
agggcgcgat	teggeaaggt	atgccccata	agctgtctct	tctttggttg	cccaaccacc	120
aatacttccc	teggggaace	tgtatcaccc	gaaaggcgat	ggctcattcc	atgaagatag	180
cttggcaccg	ggtcagtcac	cgccaacagc	ccgtttggaa	gagccgcacg	acgaaatagt	240
gaaaatccaa	acagaaaaaa	gcctgcaaga	gcgaaaaacc	tgttctttct	acactacatt	300
atttatatat	ctgcttcgct	gctctccccg	aatcctgcgc	taagcagttt	tcagaggaaa	360
cgaatgcttt	tatactttgc	atctctattc	ttgtattgct	caatgggaaa	gaatagctga	420
ccagcaatto	gtggcttccc	ctgaggcttt	agccagtacc	gatgtcggcc	actcgaaagc	480
atagccggca	agaacttgcc	caactgcatc	cccaagctca	ctcccacggc	ttgtgtgggc	540
gatacatcag	tgaggcaaag	aagcggttgt	tgtatgacat	teccategea	cgtccaaacg	600
agaactgtgc	ccgtcagtag	ctgcaaagat	agaaggagcc	atgcaaataa	cgaataaatg	660
gagcggatat	tgtatccggc	aaggagtaat	aatgccttgt	cagatctaat	atgtactgtt	720
cattgagcgg	aattgcggag	cggtcagatg	ggtagagctg	aatccgacgt	acaattcttt	780
gcggggtagt	atatacctgc	accgatgtcg	aaggcctttc	cgctcacttt	ggtagggga	840

tggccggatc gttctccgtc tcgagctcca ccttggtgcc atgaaagccg tattgacgag 900 960 teeggettgg agggegaegg acagatetee gegaagagtt tetgtttgaa ggeatattge 1020 cccatcaget cattgatgge aagagteete tegttteggt caetaceega aeteccaete catgctctcg tcgaagaagc gaataggcgc atcggccagt acgacgaaac tcttaggatt 1080 cggggcatgc cttcccattg tctattgtgc agcgcagtaa tgaaaattct ttgcgcatac 1140 1200 cggcataagc cggattgtag tagccgtatg cacggggtac tgagccagca ataaatcgcc ctgagcgaaa atatcctctc ccccgccacg gtcaggagca ggagcaaaat gagcgaacgg 1260 1320 aaagatttat gcaaactgat gccacggtgg taaaacgaag ccccgagtgc tattattgca 1380 catcggggca tattcgctta aggagattac attatcagta ctcttcttcg ttaagaaaaa atcetetttg eteggataat eeggeeaaat atettetate gttegtagat tteecettea 1440 tettecattt cetgeagatt etegatgaet caagaggage accegaaegt tgtgeatagt 1500 1530 ctatcaactc atctttggtg caggccgggg

(2) INFORMATION FOR SEQ ID NO:350

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 638 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...638
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:350

cagcaacacc	caaactggca	ccggagctga	tgccgagaac	ggacggaccg	ccaaaggatt	60
				ctgcgccggc		120
				gtgcacgagt		180
				atcggaatag		240
				ccagcgcagc		300
				agcaataata		360
				atcggccagc		420
				ttgcagtata		480
ttccttgaat	ccctgaaatc	ggcatatcgg	ctgtcttcgg	ctttcaaagc	ttcgtaacca	540
actccccggg	atagctgttg	aggattcgcc	agtagcgagc	cgaatcggtc	ggctgtagac	600
cgtctcgaag	tcgagggaaa	caccaccgga	tcgttgac			638

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 669 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...669
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

60 eggeettgtt ttegeegaae gettetttta etttggtgtg gtattggeet tgatettgae gaagattege ectaageett eteccagaga ageteetteg egaacagate ttgateggat 120 atctcatcca gacggcggac aaaagctgtg cgttgaagtt gatttgttcg cttccttttt 180 240 tgaacttatc caattctcga gcgaaacgat agggatatag atgtcgtttt cttcaaattt 300 ctctagcatt catagtcgtg cagcattaca ttagtgtcca acacgaaatt cttttttcc ctttagcagc cataacagtg catttttatg atttgaatct ttcgaaaaat cgttcgaaag 360 420 ataagetttt teategaceg tacaacegat tattettttt ttgttatata cacagegaat 480 aaaaacatca caaaaaaagg atcccaaact tcaaaaataa aatagaatga aatcggacat 540 tcagattgca gtgacatcga actgcaaaga atcgaacaga tagcagagtc aatcgacttc 600 ctgtcgaaca attagaacca tacggacgat acacggncaa agtgccgcaa gctgtatcga 660 cqaaqaqaaa gtaaaaaagg gaaatctgat ctggtgaagc cattacgccg aacaaggncg 669 tgtgggaaa

- (2) INFORMATION FOR SEQ ID NO:352
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 631 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION $1...6\overline{31}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

cctcgactct atatgtggca ggaagagcat gctcgactat gcgatactgg gctaatgaag 60 120 tacttgtagg agtctattgt aaattagaaa tctacatctc cgtttttgtc tcattattca 180 gttggctcga tgggtatgtg gcgaaaggaa aagtccgcta tagacctgac atctgtggag cgagccatca ctcttacgag tatttccgcc attcggcaca gcaagtacac gcagagatcg 240 300 caggitticag cicactcage aacageaaca acteetigee gagetaceag catetiteag 360 actgccgaag ccctgagtat tgcccaaaaa ttggggatga aagaagagct tttaaggatt 420 ttctcagtcg taatatcgga cacctctttg ctaggaacga cacggacttt accataaact 480 caatatgtaa ccgagcgcac ttctgcatta tcagcatttc gccacccctt attaaaccga aagtgtacaa gtgcagatag tgtgccattc aaatcaattt tatcaatgag caattatagt 540 600 tcaaattaga accatacaaa ggtgtgcgga cacggcatac ctgcccatgt gcgaacgtcc 631 tegatgette getegetata ttgacacaga g

224 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 638 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION 1...638 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:353 egectegatg ctettgaagg categtegte tatgtegata teettgatge ettteecaet 60 cccgggatca tggatgcaag ctctttgagg ttacccattt tttgatctga tgtatctggg 120 caaggaagtc attgaagtcg aactgatett ggetatttte teetecagtt tgegagette 180 ccgttcgtcg tattgccctg agcacgctcc acaagcgata cgatgtcccc catgccaagg 240 atacgtcggc catacgctcg gggtgaaaag catcgattgc ttccatcttc tccccgtacc 300 gacgaacttg atgggcttgt ttacgaccga acggatcgag aggcggcacc gccccgggta 360 totocatoga gottggtaag gacaacacog toaaatocaa gogtgtattg aactoottgg 420 etgtattcac ggcgtcctga cggtcatcga gtccaccacg aaaaggactt cgttcggctg 480 gatggcagcc tgatggcctc tatctcgcgc atcatttctt cgtcgatggc caaacgaccg 540 cggtgtccga tgatgacaac gtcgttcccc ttggtcttgg cttcggcttg gcgtgtcggg 600 ctattctcgg accggctttt tgcttgcccg gttcgctt 638 (2) INFORMATION FOR SEQ ID NO:354 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 689 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...689

ccgggctcga tatcgacgct ctccgcatcg tagcaggcgg ggtaaaccgc tccgctctcc 60 ggagaatgct gctattgtga tcacacacta tcagcgttgc tcgagtacat caagccggac 120 ttcgtacacg tcctttacaa ggggcgctcg tcaagtcggg aggagccgag ctggctctca 180 cgctcgaaga aaaaggtacg actggatcaa ggaagagata ggagaataat cggatatgaa 240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

ggtagagaac aatatctgca	actcttccga	gagaatcgcg	aagcaataga	cagcactccc	300
cacgggtact caatgagcaa	cgggagaagg	cgtcgatggc	tttqcctcqa	aggggttgcc	360
teggtatgge actgagaact	atcagcgtac	cgtttgtctg	aactattcgg	ttatgactac	a 420
ggagtaaacc tgaatcgtgt	catttcccaa	tcagacagaa	agaagetttt	cattgtacgt	480
tgcccggatt ggacacggat	ctttgctaca	ttgtcaatga	tgcatacgat	aacqaatqqq	540
tcgcgtatcc gaattgccgg	aaggagcatt	tgtcggcagt	ctgagcgatt	tacceteage	600
cattccggag atagcagctt	cggtattatg	ctcaagcgtt	ggacccgatc	acqatqqcat	660
tcattgcatt cagcacgatg	gttgctaag	, ,) J g	aogacggcac	689
					009

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1025 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{0}25$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

```
ctcgaatgac gtactcgtgc acgataagta tgagcaggac gtaacgctga ccatctcctc
                                                                        60
gcaatgatgg gttacacgga tgatagtatg cctatcgcct cggtgtcatc cgcgacgtgg
                                                                       120
aagcaccctg ctacgacaga gcggtgaagc ccagatcgaa gagatccagc agaagaaccc
                                                                       180
catacgcaag ctccatatct cctcatccaa ggagacgttt gggagatcaa ataaagcagt
                                                                       240
ttagagatta gtacccaaac gggtaggatt cgacagaaac ctttcgggga ggattcgttt
                                                                       300
cctacccgtt tctcttttat gggacgagtg tagaccggtt attgacaggg gtcggagatt
                                                                       360
gatcgagtat aaaagcaggg agccatgccg aagattgcgg tatggctccc tgtcagtcag
                                                                       420
attatttgtg tetgaaatae teegataega gaggagggte agtetttgge tteeataeag
                                                                       480
tecteggagg ttegagattt egaatgegee aateetgegg atatagattg ttggeaegtt
                                                                       540
gccgagattt ttcaggaagc cgagcggcct tctgcggaac gtggcgagac gaagccgagc
                                                                       600
ggcagatcgg gcatggtggt cacagactgt cgggccagta ggagagagct tcatctcgtg
                                                                       660
aaaattccat atcgaagaat gagtggcgtc catttccgtg gacaaagcca gagccggagc
                                                                       720
cggtacaaga tettteeett etgeateeee actgtgatee etgetgtgtg cageetgatg
                                                                       780
ccattgeett gagacatteg accatttega geacattggg agtaagagea tgeeatacte
                                                                       840
gtctcccatc catcgccatt cgtatttttc aggggcatgt acaagcattt gataccatga
                                                                       900
gggatatget ttetgegttt ttetttteet tetettgggt tgettatgee ttacegatte
                                                                       960
teteteeggt ttgegaacga geagaagaaa aateetteae eegcaaettt atgagggaag
                                                                      1020
aaacg
                                                                      1025
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1098 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1098
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:356

60 acatagaata ccggccacag cccaacggag atcataagga gtatgcacga gcacagcccg ccgcctaatc cgacaaagat ggacaggatc gtaaccattt gggcgttacc cttgtacgac 120 180 tgagaagett ggcaaagtaa aaacctacgg acggtagaat ttccggtcaa ttatattttc 240 cgtctccagt gatttggaga ggcttggtac tccttgtcgt tttcgttcat gtctgagctg 300 ttcagggaag ctgtagcctc catcaagagt caagacctca ccattgcaat aagcttggcg 360 agcaaaaata aaaaagctto ggotacttoa tooggtgtog caagcgatgo aaagcaacot 420 tattctcgat atttcggcgt atttcggccg gttgttcttc tgccattccg tatctacaaa teceggtgee acggeattea eeggatgeea taaggeteea gatgetteae eagattgegg 480 540 gtcagagcgt tacagcggat ttgctcactc cataaggcag agccatgccg tgcggttctt teccatgage gateeggtaa agatgataca teegttgttg egetegateg eggeagaagg 600 cgttggatca ggaaggtggg gaaatggaca ttggcaagaa tacgcgctgc cattcgtcga 660 720 tagtcatctc ctcgaaaggc gtgcggatgt gatgccggca ttcatgataa gagcttgcag 780 agtaatatcc ctctgtcaag ggcttccgct atcaggtcga tacctttcgc atcggtagca teegttgeag cagetetaeg gatggagege tetetgeeaa tteggeegee aetetegege 840 900 cgtctcctga tcatgtccgt aggtaagaac gagggagtat ccctgcttgc caagagacgg 960 gctactgcga gaccgatccc cttggttcct ccgtaatcaa cgcgtatccg accgccataa 1020 ttcctacatg ttttggacag cttgggcttg tgctgacgct cttcattcag cgtcttggca 1080 tagctatcgg tatagtctcc ttgattttgg tagaggaaac gcccgtcccg taagggaata 1098 aaagacctga acgccgag

- (2) INFORMATION FOR SEQ ID NO:357
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 927 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...927
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:357

tttgaaggtc aggtt	ggcca gtaaaagcag	aattagaggc	aatgcccgac	ctcacggtag	60
aataccattg ctgaa	geegg eteceacact	ggtcagtaga	cgagcatgaa	gataccccaa	120
aatacaccga agget	gtggc cagactggtc	tgcgattgct	gtagatcgta	tgccagatct	180
ctatccaacg atctc	ttcga aaaatctcat	agtctccttt	ctcctccttc	gtttagtttc	240

tcatccctcc	accgcgggga	ttcgtacggc	tttgcgggcg	ggttggtatc	ctgcatggca	300
ccgcttacta	ccatgactat	cagagctaat	agggcagtgc	tcagtcgatg	ctcggatcgc	360
			gttgctcccg			. 420
atgcgatacg	aactccatca	gccaacgccg	gccaccaagc	ctatcagtcc	ggaaaacagt	480
gtgaccacta	cgcctctgtc	agaatcatgt	tgatgatagc	tcttggcttg	gctcccagtc	540
tttgcgaatg	cctatttcgc	gctgtctttc	attgacggtc	acttgcatat	attggccact	600
ccgataattc	cgatgacaag	ggtgctcaac	ccgataacca	aagaaaaaca	tccatgccat	660
tgaatatctt	gtccatcatt	tttatgccgt	caccggtgca	tcgacatagg	gcacttccat	720
atcggtagga	tcataccctt	gcggaangcc	agttggcgat	tgagtagtac	tttgagtctc	780
tcacttctct	cagttcgcac	agacggcagt	tcatgacagt	gtgcagtcca	gacgaacctt	840
tggcgaaaat	acctggatag	gtggcgaaag	gattagttgg	gcgaatgccc	tgtcgccttg	900
caacgctaca	cgaggaacgg	atttgga				927

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...622
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

```
60
cgttgatcga tttcttgcgt ttcggtgcct actatgcggg ccagatctag ccgatcaacc
                                                                       120
catcagtgag aaaggcattc tcaatcgggt ggagtacctt cgctcgaagg tttcgttttg
                                                                       180
geogttacte ctttcaattt caccagtttg cttccaacct gaatetggca ceggecatga
                                                                       240
tggggaatac tactattgga agcettecae tacagetett catageaact aceteettat
                                                                       300
gaaaacttcc aagaggccgg tttgcccgat ggtgtggtca atttccttcc cggaagggta
                                                                       360
gettgategg tegggtagee aeggegaaeg aacaettgge eggtteeatt ttaceggtte
tactgctacg ttcaacacgc tgtggaagag cacgccggca atatagatcg ctatcgtggc
                                                                       420
                                                                       480
tatccccgta tagtgggcga acgggaggaa agaacttcgt gatggttcat ccctcggctg
                                                                       540
aagcatgcga gtggctacgg ctcttgtgcg cggagctttc gagtatcagg gacaaaagtt
                                                                       600
teggetgeaa gtegegeata tatecetegt tetttgtgge eeagegtgaa gaagtgatgg
                                                                       622
gcgatatgct cgacagtatc aa
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 587 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...587
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:359

toccogogga agatttggca goctatttgg gtgtaaagca tgtaatccct gogccaatgg 60 tacaqacqca ttqcaaatca qtctqatqqc tttqqqatqa aaqtcqqaqa tqaqatcatt 120 gtgcccgatt tcacttatgc agcaagtccg aagctatagg tttgttagga ttaacacctg 180 ttttcgctga tgtagaccta ttacatttaa tcttacatct aagggctgcg aaaaagttct 240 gtccgcaaga cgaaagcaat cataccagta cacctctttg ggcagtcctg cgattggagc 300 cgcttttggc ctttgccaag cgaaacgatt tgtttgttat cgagacaatg ctcaggcaat 360 gggaggggga tatactatct ccgatggatc taccgaaaaa caggaacaat ggggcatata 420 480 ggctgtgctt ccttctttcc acgaagaatt tgggttgtta tggagacggt ggtgctgtca caacaaatga gacgaattgg caaagcgagt gcgaatgata gcgaaccatg gccaaaagac 540 587 aaatacaaac atgacattat cggatgcaat tcccgactcg atactat

- (2) INFORMATION FOR SEQ ID NO:360
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 826 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...826
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360

tcaaccggct	atcggtaagt	aggaatcaga	ttcagcatcc	gataaagagc	gagcgtaact	60
				gatgcccaca		120
				acttctttga		180
				ctttgcccag		240
				gatcgtcgta		300
				atcccttgct		360
				gccactctct		420
				atgcggtact		480
				aagagagaat		540
tcaatgccga	tatgaaaacc	agcaccgtga	tcaccgacag	aaagcgaagc	gaaaatggag	600
ccgatactgg	acaaaacgaa	ccagaggcat	cagcacaagg	caagaatcca	agagagacaa	660
				aatgcctcca		720
				ctgtcaaaaa		780
		gagtgagttc				826

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

gtcagctgct tgccggaaaa aagcccagta cgcgtcggta acgaaaaaac caatgccgaa 60 gagtaatgcc agaccgacat attgggcaag cgatcgttgg cggcaaagcc ttccactctc 120 atatcaagtc cctgtacgaa gaaaatatca ggccgatatt gaccatattg gaaccgatgg 180 ctacaaccat cggaaccgtg tgtcctgcat ccccacatac cagccgttga agacatagac 240 gagcaggctg cgggcgctcc ccacagagcg atgcggatat attcgcgtgc ctctgtccga 300 tggtctcctg acccgaagcc agcagatacc cgaagcgttc tgtagaggag ctgctatgag 360 aagaagcagg gctgcgacaa ctgccatcgc gagccacgtg ccagatagcg tgtgatggct 420 cgcacatege tacgcccgaa acctgtgccg tgaatcccgt agtccccata cggaggaagg 480 cgaagagcca aagacgaaat tgaccacccc cgaagccaca gccactgccc cgatagagtg 540 gccgtgtcca tacgaccggc cagccctaca tccacgatgg agaggagcgt acggtaatgt 600 tggagatgat attcggaata gccaagcgca ggatgcgctg ttcatcttac gccccgcggt 660 cagtcgcatg cggataggga ggagtttcat gaggttcggt cagataggaa aacagtccgg 720 ccgtgcactc ttccaaatgt ccagcaccag ctcgaagccg gatgctcctc catagtacgg 780 atcgggacat ggtcgtgaat accgctactg ctgaaatccg tcatcagacg gatttggccg 840 cagcetette ggteggagee agttettgea geegeteteg atggeaaagt ceatgeegat 900 gatataatcg aatcgttcga aatcctcata cccaccggac gggagagcga agtgagatcg 960 tageceegge gageagegtg geaegeatte gggeategge etttteecee tgatggtaat 1020 tgctcagtcg gccgaatcga tgtggaagcg atcggcatgc ccctgctctt ctacatacag 1080 cgaaagacag cctcggcaga cggagagcga cagatgttgc cgagacaacg aataggattt 1140 tatgtggctt cataagcgga ttatcgaagc aaaggtgtcg cttggtacgc agtcgcaagc 1200 tgttggtcac caccgaaata ga 1222

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...488
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:362

cggcaaacat	cgctccggtt	acgaatatgc	ccagatcctg	agtggagaca	gggacatcat	60
tccatccgcc						120
ctgcgaagca	tttccaagcg	caaagggttt	tattgacttc	ggtcttggtt	atctcgcttt	180
cgtccagtcc						240
tataccagat						300
ccagccggaa						360
catggcttgc						420
attcaccgtt						480
atogtaaa	333 2					488

- (2) INFORMATION FOR SEQ ID NO:363
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 725 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...725
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:363

gtatcggaag	gccgcaaccg	caccaaggca	cagatcgaca	gcatcgctca	ggccgtgtat	60
ggctcggcga	caaagctctt	gcactcggtt	tggtggatag	cttggaggtt	tggacacagc	120
		tggctcactc				180
		gagttgctct				240
tcctggtacc	attctctccg	atccggaaat	agaagttctg	cgcgaactcc	gctcatgccg	300
ccccgtcctt	cgggcataca	ggcacgtctc	ccctattact	tcagccgtac	tgataaatga	360
gacaaccgta	attgctgaag	agatggatgc	gcccgtatca	acaagtggct	caaaccgctt	420
		ctgaggttgc				480
		ctatcgtctg				540
		cctgattcgg				600
		aaaaccaaag				660
		ctcgtcgatc				720
qtqqa						725

- (2) INFORMATION FOR SEQ ID NO:364
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 656 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...656
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

cccagaaaaa agaatctgtc ggtagagata tgtactgaaa tagagtgtgc agttgtgagg 60 atagecatea aaageeetta ttaateggga tagteeagte ttataggtet tataagattt 120 attaattoat tggagagaat cagatatgca ctgtattgaa gtoogottga cttttttoaa 180 aatotootat otoatatatg caactootot accattatac ocaaggatgt atttatogto 240 taatttattg cctgagaata gtctttaatc gcttttttat accatccttt cttaaatatg 300 cattteetet accatgatae geagggegt atttategte taatetattg cetgagaata 360 gtctttaatc gcttcttcat atgatccttt ctacaatatg catttcctct accataatac 420 gcatgggcga atttaccgtc tattctattg cctgagaata gtctttaatc gcttttttat 480 accatecttt ttagaatatg cattteetet accatgatac geaggggegt atttategtt 540 aattotattg cottagaata gtotttaato gottottoat acgatootto toacaatatg 600 caactectat accattatac ccaaggtgta tttategeta attetattge etggag 656

- (2) INFORMATION FOR SEQ ID NO:365
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 890 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...890
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:365

cgccggtgaa agctgtgata agcgaagcag ccaagccgaa tggagcgata tcttgatgtt 60 tttgagagca aagteettgt gtttgteate etttegeaca ggtagatgee acataegeee 120 aaagcaaata cggatccgag agtccagagg aagagatcgt gtgccagaac ttattgatcg 180 cagtggaaga gaatacaaag cccagaaatc cgtcatttcg tttgcgcatc gtatcggggt 240 tgaagtcatt cctaccggct cctgcatcca tgcattggcg ataagaatcc atacgctgac 300 aagctggctc cgatgatggt cagccatgtg gcacttaggt gaaacctttg ctcaccttgt 360 tccagccaaa gaacataacg gcaataaaag tacctccatg aagaaagcca aaataccttc 420 gatggccaat ggcgctccga aatatcgccc acaaagagac tgtaattaga ccagttggta 480 ccgaactcga ttcgagaatg gattcctgtg gccacaccga tcgcaaagtt gataccgaaa 540

gcttctgcca	gaactgagca	taacgcttcc	actccggttt	gccattgcat	aatagatggt	600
			cagtgtcgcg			660
			agcttactaa			, 720
			ttccacgttt			780
-	-	·	cctgttgctt			840
			gtttgatgag			890
-						

- (2) INFORMATION FOR SEQ ID NO:366
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...508
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366

egeegettgg atetetteat	ggtcagctct	ctggacaagg	gcggattggt	togggtggta	60
ttttctctat tgctttcgat					120
cgtctcttct cccttgatgg	ccgacgcatg	aaacggaacg	atctggtcaa	agccgacgaa	180
ctcttcaagc gcgtctgctg	catcagcttc	tttccggtgg	ccttatcttc	ttgcttattt	240
gggtcaatat cgacagcatc	ttctccatcc	tcccgaacgg	tcacctctat	gccgcggcaa	300
atatgtcgtt ttctatttgg	gaatcgctaa	gatgatcgaa	atccgctgaa	ctacggcaat	360
ccgatcgtga gctgttccaa	gtattatcac	tgaatcttta	ctatactttt	cctcgtcacc	420
cattctggcc cgtgctcacc	atctggtggc	tgatcctggt	tttgggaatc	aacggaccgg	480
ccatggcacg tcttgaccac	gctgcttg				508

- (2) INFORMATION FOR SEQ ID NO:367
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367

cgctttctcc	cgtccgcgtg	ccaatggtgt	gatcgctatc	gacctgcgaa	caacgatggc	60
		caatggtaaa				120
		teegtggteg				180
		tggtcaggac				240
		ggtagtaagt				300
		tcgcggtggt				360
		attcgagccg				420
taagagcggt	gtcgccatcc	ggtaaaagtg	gctgatctga	gcattatcgg	tcgagctaca	480
caaggtgtta	gctcattgat	ttgtcc				506

(2) INFORMATION FOR SEQ ID NO:368

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION $1...5\overline{39}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368

cccctctaac gatgatgccc	tgaaggctat	cgaactgatc	gtaggcacgt	gtgccaggct	60
atcaacgaag gtctgatgga					120
cageteeecg tegegaacgt	cgcgctcctc	aggagctcgt	cgctctcgtc	agaatgagaa	180
cgaagctacg gcagaactgc	cacagaggta	gcagaagctc	cggaagccga	agaggcggaa	240
taaacgcaca catggaatta	tgagctatgg	gttataatcc	atgagtggcc	tcagatgcag	300
gttccaaact caggggttat	gactcatggc	tcataacttt	tttcagaact	aataacccat	360
tcattataga acaaaccaat	ggctgtaaca	atcaagacat	tgccaagctg	cgtaagatga	420
agcggtgccc gcatgatgga					480
gaaagccatg gaatcattcg	caagaaggac	cagccagtaa	gcttgccaag	ccgttcgga	539

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...513
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:369

ctcaccaatt	tttatttcac	ctatattata	gtggtcgtcg	atgttaccca	agcaaaaatc	60
gtatataagc	cgtctttctc	caaagggatc	agccattctt	tgcagctgac	aactggacat	120
cctcaaacac	attggcactg	cgaaggaacc	atccttatcg	aaagcataaa	cgttcaatcg	180
ggcaacttcc	gcaggaaaga	aggattttcg	gcacactcag	tctgagaata	gaagttgaca	240
tataccctcg	aggacaatca	tcgtaattgt	cataaatcat	cttatcgcac	gaagcaagcc	300
accccacagg	gccattattg	ccggcaaaga	aataataagt	ctggaatatc	catatgcttc	360
cgtttgttca	ttgttttaaa	aaatatagag	gggggagaac	ggtgggaacc	gaaatcccac	420
cctcaaaaag	aaaattttac	atagctaatt	agagatcaac	ctcataggaa	tgaactttcc	480
aaggcaaaac	gtaacctaac	cgacatgaac	gtt			513

(2) INFORMATION FOR SEQ ID NO:370

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 586 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...586
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:370

cagaccgata	cctacggcac	cgaagctgcg	agctatctcg	gcatcgtgag	agtatcggca	60
ttcgtacgaa	ctttcagctt	ggcatactta	tcggccaagc	catcagatcg	gcgaaatctt	120
gatccatttc	ggcggctttc	gtctccactg	tccttcgtat	atctcaccgg	tagaaccgtt	180
gatggagatg	tagtcgcttc	tttgaagagg	ggttccatcg	atctctacgg	tacgtgcctt	240
atagtgatgt	tcaatgcacc	tgctcccgat	acgcagcatt	tgcccatacc	tctgccacta	300
cggcagcatg	cgaagtcata	cctccgcgag	ccgtcaggat	acctcggcgg	cagacatacc	360
ggccaagtct	tcgggcgaag	tctcgatacg	cacatcacca	cacgcttgcc	atcctcttc	420
cactgagcgg	catcgtcggc	gagaaaacga	tctgacccgt	agcggcaccc	ggcgaagcag	480
gcaagccctt	gtcagtacac	gtgctctaag	gagagcagac	ttgtcgaaaa	tggggtggac	540
aattcgtcca	gcttggtagg	ttcgacgcgc	ataagggctt	cttcct		586

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1949 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1949
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:371

acgtccataa tggtgctcac tgttgtgacc tcccattatc cgcccgaatc atccaagaga 60 120 ggttgaagca cagccctgaa gaggctgtcc ttgtgctcaa gtagttgtat atattgctca 180 cgggctactc ccgattcgcg agcgatgttc ggagagaagc atctcggaaa ccattgacca 240 taaattooto togtgogoto goaagattot ggoacgagoa tocatotogt tttttgtoot 300 cgtcatttga tctcattatt ggtacatgac aaaggaacaa agcctgaaca gtgtcacaat 360 cccgtttttt aggtaaaatc gagcatgaaa gcggctgaaa gctacaacaa atcggcaaaa cggctgttca taccgatctg tacaccaatc attctgatgt gtacgggaaa aaagttgata 420 480 ctcagaaagg tcaaaaaatc ataatcgtgt cgaaacattt gaccgattcc gagcgtcttc 540 acattttgag ctgttgcaca ataacctccc acctcctcat atcgatcaag acagacacag 600 cattgatttg acgaagaaag gagagettca tgcgatetet etgcaaacte aagtaatetg aaaaacactt aagaatcagc tctgcggcaa aagacttaat aaaagtccta taaaatagtt 660 gcaaatagct gatagttagc gcattgtggg agcagaatca agctgacaat cgcgtcctgc 720 780 atogtgcagg aagcagaatc agccgacaat cgcgtcctgc atcgtgcagg aagctagaat 840 caacgacaat cgcgtcctgc atcgtgcagg aagcaagaat cagctgacaa tcggtcctgc 900 atcgtgcagg gagcaagaat cagctgacaa tcgcgtcctg cacgtgcagg gagcaagaat 960 cagctgacaa tcgcgtcctg catcgtgcag gagcaagaaa cagccgacaa tcgtttctta tttctcgcct atttgacgag aaaggagtac ttctctaatg gaaacttggg gaaatttctg 1020 1080 tttgctcgag tccatatacc ggaggtttga tctttcccaa aggcactaag aatcagcttg 1140 cagcaaaaga gttcaatgaa actcccatgc aacagtctct accggctttg atcgtcgatt 1200 ttttttctcc gctttttcgc tgatcgggca gaacgaatct atgacctcgt tcatatcggt cgtatatctg cgcgaacgat gcttgtcgaa gagacagatg ctatagcttc tgtttcttgg 1260 gtagcaacgg tcagctatct cttccgaaac gctggcggat cgcatccaca gaggataaga 1320 aacctcctgc cgcatgcgat cgatcgggtc gaaaagattg agctgatagg ccccgctacc 1380 1440 aagtoggaca agatoaccco tgootgtttg tagggcagat tggtogataa atotottgta 1500 gcagggtgcg aatctttggg atcagttctg agggtcagaa gtagctacgg gaaggagcat ctcattccgg ccggaatagc gttctcctga tcaaatcggc tacagcttat aaagatactc 1560 1620 aaacggcggc cctgctcttt tcttcacgta tcttcgtaca gcaactatcg gcgaaaaagc 1680 caaatgcctg agaagggagt caaaatctcg gcatggatgg ccgaaaagcg cgtggtgcag 1740 acactttggc gaggctgtgg caatttcatc tctttcaggc ttcgccccta agctcctgcc 1800 atgtcctgac gcccgaagtg ccggcaaacg atatacccga ccttctctca tcgaagcaaa 1860 gtcggctgcc gtatgatacc ataatagtat agcttgcgag atagtctgcg ccctattccc 1920 caacateget tacategaac gtttgcagag cettteteet ettttetteg ggtetatgge 1949 gcatacgccc ttgtaacccg catacctct

- (2) INFORMATION FOR SEQ ID NO:372
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 671 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...671
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:372

cggtttttct	tttttgcaga	aatgcaatgt	caccaagttt	aaagggtcag	tcgctgcaca	60
tcatatacag	ctatattaat	tccatggcca	gtgccggata	aaaatcattc	agctcttgtt	120
ttaaaatctc	ggcataggcc	aaattttatt	attagttgtg	tgccttagca	actttgattt	180
		tatctgtccg				240
		gaatggtatt				300
		cttaataaca				360
		atgatgaaag				420
		agaagttgtc				480
tttaaaaatg	gcaagtagtt	tcaaaatatt	ttcatcagat	ttttcggaaa	taatacctag	540
attcccttaa	aataagaaca	tcgtaatcca	aaaaagnagc	ccggagtttt	ttctggactc	600
ctcattcaat	aatagtgagg	agccctatat	gcatcaaata	tcctaatctt	ctgaaaaagg	660
aattgtatct	a					671

- (2) INFORMATION FOR SEQ ID NO:373
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 542 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...542
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:373

```
ctgcaaggcc gtatctatgg tacgaaggag ccgatcgttg tcccatggct gcctatgaag
                                                                        60
togaaagoto caagootoat toootooaot gooagtggat ogaagoocaa googtoatoa
                                                                       120
gtatgacagg gcaggaagtg aatatctcat cttctccagt agttccaatc cttccctgcc
                                                                       180
ggaggtcgaa agggagaatt catatccatc agaatcacag ccggcttaca gccgccatca
                                                                       240
ggattcgcat tatggacaaa gcttcgtcgg gactgttggc tataacggga ttatgcccgc
                                                                       300
tcgcttgagc accagacgca gtgcggcaca gactgccaca tcacgtctac gaccaaaata
                                                                       360
tcgatcagtt tttccattgc acggtaaaag taaaattggc gttgaagcac ggtctttct
                                                                       420
gtcgaatgtc tcaatcgaga cgttgcaggg gattttcatt gaactctttt tccgcagagc
                                                                       480
tgattetttg geettegtga aagggtaaac etceaggaca tgageacega geaaatagaa
                                                                       540
tt
                                                                       542
```

237 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 497 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION 1...497 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374 60 ggtttcggcc gacatcggac gggggaaagt ggatttcagc ttgtttctca ggaatccggt 120 agtacggatg ttgtatctca gatattcgat acagaaaaat gtcctcttat ttcttccaac tcaaggaatt cggcgaaaag atgggaggga agtacccgca ggaggatggt tcgaacagct 180 240 actteggate eceggateat teagatagat gaagataaag aagaagaaat teeagaagat 300 gaatggctgt cgtaattgaa acttgtcgga gagcccttga tcagctaatc ggatccgcga 360 gcaggagggt gctatgctgg agcaggtgtt cacggagaaa atactaatat ctcttctttg 420 cttctgcaaa tcgaacagta tgaacccgat agatccaacg aatcaaagag cggatagaag agaacctaac caaaatatca ggaaagactt ccaccagaac ngattcgaac caagagatga 480 497 tttattatat gaaaggt (2) INFORMATION FOR SEQ ID NO:375 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 518 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...518 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375

gatcgaaatg tgaggctaaa ttgtgcagat actcctccag caggttatag catcctcgtc 60 gatgtggaag accttgctc ccagattcat cgtgagcgtt ttttcatctt gtttttccgt 120 taatagcaga ttcttcttcg ggcttaaatc gcgcaccaat agttgcaatg atttgttgcc gttgaattcg ttctctctat cgtgtagcaa agacgaaatg agcccgtttt tgatctcatc 240 gcaataccgg cctgattaaa cgcaatccca ctcaccggat ggcgttcgcc cgatccactc 300 tcacatctat cttcaggtgt tcggaagctt ttcctacagc cctctaccac cggcatcata 360

cagttgtcgg	gatataaaga	ccggcttgga	gtttccgggc	cgaatggccc	cateegettg	420
aggttgtcga	gaagtttgta	atgacctctt	cgatggatat	ttcggcatct	acatctattt	480
gtggcaccaa	agttccggcg	atacagcctc	ttcqqcat			. 518

- (2) INFORMATION FOR SEQ ID NO:376
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 558 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...558
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376

gccacgtgat	ccaaataccc	acggacgggg	aaaatgagat	agagatagcc	gtttcgcgaa	60
tgcggtcgaa	tgcgaagtgc	tggatgatgt	gtatcgtatc	ttgagcagaa	cggcggcaaa	120
agccgagagg	ataccgatga	tgaggctaag	atgatgagaa	aaagcctttc	gtttatgtgc	180
ctttcgcgcc	aaaggagaag	tgcaagaacc	acccgtagcg	actcgtttcc	ttatccttca	240
tttcccaatc	ctttaaaaat	cgtttggcaa	gtatataaca	gtacttctat	atccgcctga	300
ggctcatatt	ctcgtagtac	agaaaatcgt	attgcaggcg	ttcagcattt	catccggagt	360
ggaagcatag	ccgtatcgta	ccatgcccca	ggggtgatgc	ccggacggac	attgtgcagc	420
				gaaagcccgt		480
gccccacgaa	ctcatatcgc	cccgaagcac	attccagaac	tgaggcaatt	cgtccatccg	540
tatttgcgca						558

- (2) INFORMATION FOR SEQ ID NO:377
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 646 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...646
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377

tggttcggac	gacctttttg	gttttcctca	cttattccgt	cgtacagctt	cgttctcgct	60
gatgcaggac	ggtcgggtag	agatgggaga	cgggctgaca	ttctctattt	cggtgtgaat	. 120
ctgatcttcc	tcatgttcag	ctacctgtcg	tctatctgat	ggagcgtgct	ttcggctacg	180
tttccaatat	cagtttgttg	agctgagcga	cgtcaatacg	ccgctgctca	gtcagctctt	240
			tcgatccaag			300
			ttgtacgcac			360
			aggaatcagg			420
aaattgcctt	ttgacgagag	tctcgcatta	tcattcgtca	tgtgaccgat	ggtattgcct	480
tggcgcagaa	caccgtttgc	cggactccgt	tatcgatttt	atccggacgc	atcacggacg	540
ggtaagacca	aatacttcta	taattcctat	tgcaatcagt	atcccgacaa	gaagtggatc	600
ccgagttgtc	acttatcccg	ggcccgaatc	cattcaacaa	ggagac		646

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 710 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...710
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

agccgacgta	cccttaacct	atttccacac	cgaccacaaa	gatctgatct	gtccagccct	60
			aatgccgaaa			120
			ctttgccaac			180
tgcgaatgcc	acgatctgct	caattccgag	atgaagaaaa	gccagaccga	tgccccttgg	240
			tcaccttcgg			300
aggacttgaa	gtgatgctca	acggtcgctt	catgggacgc	aggtcgagca	aaactggtat	360
gcttactacc	ccgaagttcg	ccccgaactc	cacaactgct	tgcagcagaa	gagcctgaat	420
tggctgctca	gggactgctc	ctcatccgca	agcaatggtg	ttcaatgcct	ctgcttacta	480
ccacatgaac	agtatctcac	cttcggtgtg	aacttgaaca	acatcttgga	tgagctttaa	540
cggagaaaga	cggctaccac	atgcccggac	gtaacatcat	gggtaaggta	tggtcaactt	600
ctaattctct	ttcccgagag	cagatataaa	agggagcggt	ctccctgcat	aatcctcaca	660
gagcaaagcg	gatattcctc	tcatacgaga	agcgggtatc	cgctttctga		710

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...789
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:379

60 qqactttaga agaaacactg taattttaat cacgaatcag acactcttta gtgtcaaact ttttcagtac acgtcacttc ccttttaggc aatcaaaaca ttcgataaat gaaaaccctg 120 ataacaaatc gtttcctcct gctttttct ttttgcttac tgctgtttct gggcaggggc 180 240 aaqaagtcta ctatccgggt ctgtggtttt tcctgccgat gccactttgg aacagaaggt ggagaggcgg caaaggtagt ccctacccta caacagctgg cttggcagca gatgagctga 300 cggcatttct gcacttcggc atcaatactt ttaccgacag tgatggggtg atgggaaaga 360 420 agateeggea etetteaace eggtggaget ggtgetegge aatgggtaeg aataetgeae gaageggget ttegeatggt atcettaegg ceaageacea egatggtttt tgtetetgge 480 540 ctacagccac acgcgccatt cggtggcttc atctccgtgg cgagagggca aaggcgatgg gtgaaagaag teegageage gtgegaagag tatggtatga agtteggett tatetgtete 600 cttgggatcg caatgcggag tgctatggcg attcgcacgt tacaatcggt tttttgtcag 660 720 tcagcttacc gaactgctca ctcacttgga gaagtaccac gaagtatggt tcgatggagc caatggcgaa gggccaacgg caagcgacag gaatatgaat gggagacatt ctacgacacc 780 789 atcccgact

- (2) INFORMATION FOR SEQ ID NO:380
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 871 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 - (-, ...-
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...871
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:380

caactttaaa	ggatccccag	cattcctgcg	caatatggta	cataccatat	cggcacgctc	60
		gctatccatc				120
						180
		teggetegge				240
		acagcaccgc				300
		tegettegee				
		gtacacctca				360
		ttatatcccg				420
ttcgaacttt	gctttcatcg	tggattgcct	cgtgtcagtt	tcttgatggt	gagggcttca	480
gccttgtcgt	cgcaaggcgg	aggttgtact	cgctgccgac	caaggcttct	ttgattttat	540
		ctatctcgtc				600
		ttcccgaaaa				660

cgatggattg tttctgcgcg atggcagctg ctgtctgtac tccagaccct ttttggacgt ctgcaccagg agggtatcat cggaatgaaa aactgcggac gaatcacata catcttatcg tatcgtagga catatccaca ataccgccgt tgtacaactc gttgtccggc tccgcagaga gacgagtacg gcaaattcgc aacctttggc c	720 780 840 871
(2) INFORMATION FOR SEQ ID NO:381	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 239 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
(vi) ORIGINAL SOURCE:(A) ORGANISM: PORYPHYROMONAS GINGIVALIS	
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1239</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381	
acgctgtcgt ttttatttca attgcaccat acaggaatta aaaccgcctt atgctcgacg acgcagacga atcggatcat ttcaattgca ccatacagaa ttaaaacgct ttggctgcga attcccttac gggccaatcg aagatttaat tgcaccatac aggaattaaa atgtatccat tatactactc ccaaaactga caactagttt cggggttatt tggcttgttt tttaggtat	60 120 180 239
(2) INFORMATION FOR SEQ ID NO:382	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 726 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1726</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382	
cgtggacgta gctctcctct cgggaggtat atacgaagcc ttggtaacgc tgtaggcggt ctcgttgtcg gtatcgtaac gctttttgcc tacaactact cgtagctcag gtggataagg tcgtcaataa gatggaaacc aagactctga gtttatggat ctccttaacg aacccatcaa aaaatgagtc tgaaactaaa accaaggtca cagaagtttt tagcatggct tctatgaccg	60 120 180 240

acgtgttttc	ctgctgctca	tcttcttcat	ggtgaccagt	acgctcatcg	taccaatgcg	300
ctacgcgtat	ctcttccctc	tgccaataaa	cagcctgccc	ccgagctcct	ttggcacgga	360
tcaccatttc	agaagatatg	cgctatttcg	cccttttggt	caggacaaag	ggcatgaggt	, 420
cgctttcgag	gagatacttc	cctcttgctt	caggagcaaa	gtcgcaatcc	cgaaatgtac	480
gtagccatat	tgccgacgag	aatgtcccgt	atcgtgagat	cgtgaaggtg	ttgagtatgc	540
cggggagaac	aagatgaaag	tggtgttggc	caccaaagcc	caaagtaaaa	gtaagttcat	600
gcaacaagag	aaagtcaaac	gccaatgccg	tgccataccc	gtatcggtgg	ggggcacatg	660
tcgcactgat	caccctcttg	tcgtgcgcat	cttcgtgctg	gttcgcgccg	aagaaccgga	720
agaact						726

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 697 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...697
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383

```
60
cggacttccg ctaatgtttt ggagaaaacg gccggatttt ttacaaccaa gagagtgcga
                                                                       120
tagectgatt atcategtta tgttecagae tgtecatete tetttetett tggecacaet
                                                                       180
gatettgaaa atagetegta egateagatg gaegeaataa teeceaceae teegagegga
                                                                       240
taagccacag cataacgagt gtgatagtcg gatcgccggt tcccgttaga tcatggaatg
                                                                       300
tetgeeggea geteecagge eeggtgtgtt egtgaeggea eeggaeagaa ttecaccatt
                                                                       360
gtggacatgg atatgcctgt cacgaagtgc agaatcaccg ttgcagtacc cccagaaaga
                                                                       420
cgacgcccat agccagtagg ttcaaggtaa gcccccttg cgaagagagg agaaaaaacc
cgggcccact tgcatcccca cgagtaaacg aataggatca gtccgaactc tttgaagaaa
                                                                       480
                                                                       540
tgatgtacgt aggatgcaga ttcatgccga aatgtcctaa gactattccg caaaaagaag
                                                                       600
aaagtaaccc ccaaagaaat tccgaagatc tttatctttc ccaaccaatc cctaaggcaa
                                                                       660
tegttaegge gaccaagaga atggagtgee cacteeteae egaaageaag teattaagee
                                                                       697
attgcatatt catccaaaca gcttatgtag tcaatag
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 874 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...874
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

ccccggcggc ggtcaatcgt ccgacccttg tcctgagtca caacaagact tggcagcaca 60 gctatacgga gagttcaaag ccttcttccc cgagaatggg tggagtattt cgtcagctac 120 tacgactact atcagecega ggeetactee eegteacaga cacetatate gaaaaggaca 180 tggccatcaa cgcggaatcg aaaaactgcg attgagggcc acggcttcgc tcctgtcagg 240 gcggaagaat gtgcttgtgg tcagctccgt atcctgtctc tacggtatgg ccaacctgaa 300 gettttteeg aaaaggtgat cageetgeac aegggacaaa gggagacagg gateatttta 360 teegeetget ggtagagage tactacacga acataaagta gagttegaga geggeaactt 420 ccgtgtcaaa ggcgacagcg tgacatattc cccgccgtag aaggttatga cggcgtggca 480 tacagggtgg gttttgggat ggagaggtcg agcggctgag taccttcgat ccgcgaacgg 540 acgggaatac ggcctgctgt cggagctgaa gatatatccg gccaatcttt cgtgacgact 600 aaggagcagg tggatcgggc agtagggaaa atcgatggga tctgggcgca caggtcgatt 660 ttctgaaaga aatcggcaaa ccatataagc caaacgcttg tatgagcggg tcacgtatga 720 cttggaaatg atccggagtt gggttattgt tccggtatta gagaactatt cgcgctactt 780 cgacgcccgt gacgcgggcg aacgtccttt ctgtctgttg gattatttcc cggggatttc 840 ctgttggtca tagacgaaag ccatgtaacg atac 874

- (2) INFORMATION FOR SEQ ID NO:385
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION $1...6\overline{30}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

ccgacctttg tttttgcgtg aagtgggatt ttcactacgt cgcccgtcga atctttgcga 60 cgagcggaaa agttcttatc tccgcctttt ttccccccgc atagtctttc ttggtatccq 120 catactetac atggatgcgg cgaccatcac ttcgtaccga ttgagggttt ctactacgtt 180 cttggcttcg aactcgctac atcgaagaaa gcgaatcggg gcatcaggtc gatcccgtcc 240 cgatatgaca cgccccggga tacaacggtt gatcagctcg atcagtcggt tgggaacatt 300 tgatccatct tgccaaaatt gatgaacaga cgggtcatcc cttttctgct tcgccggctc 360 ctcgttttcg gtttttacga tctcccgaaa cccgtctttt tttctctcga ccacttcttc 420 cacgtcttcg gcacgttggt atagtcgagc atgcgattga actccaatgc cattacccga 480 cgaatcaatt gtctttttca atccattcga gcttttgntc acttcgttca agacagagtg 540 atggccgttg tgttctctat atccacacgt tctatacgat cggccagatg aacagttgct 600 tttcgcatat ctctgcttcc ggaagggatg. 630

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 697 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...697
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386

60 ctgacatccg ctcgaaccat ggacacctcg tctatgataa tcagatcgaa cttcggatca gtttcttgtg ttcgttcgtg tagcgaaaca catcgaaccc cgtctgtcac gagtactcaa 120 180 atcgggatcg ttcggcggaa tcgggcgaga ggcagtttga aaaacgagtg gagcgtctgc 240 cctccgacat tcagtgcgca aggnccggta ggcgcaagca cgacaaactt cttatgcgtc gtagccagat atgccgaagc agtgtggact tacccgttcc ggccttgccg gtcagaagag 300 getttggtet gtgegttega teaggetgag cacatagece atcecteatt ggeaaggteg 360 420 attgcggaca ggccctcctc tctcttttt gtttgcgacg aggcatgcgc tcaggggcgt ttgtatcggg ctttgacttt cgcttggccg gtttgctctc gttgtggaag cgatctacgg 480 540 ccgtcaccca taagtataat cggctgaagc atgggaagtc gggaaggcga atgctgtttc gggagtaatc acccaaatgt tttcagcttt gntggatcgt ttcttcatcc atgacggaag 600 660 gcatagacca cgaagtagga agctttgaca gggtcggatc atcctttcag cagccnaatc 697 aggtgaaaac tgatggcaac caagcggatg cagcctt

- (2) INFORMATION FOR SEQ ID NO:387
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...633
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:387

accgattata	tcagaataaa	aacaaatatt	gctttccaag	ccctgcaagc	catctctccc	180
atagatggcc	ggtatccaac	aaagtagaag	tacttagtcg	ctattttca	gaaggatete	
taattqctat	catataaaaa	tagaaataa	atetttasta	gatatttaa	atgattgcct	240
tcactaaaaa	atatataccc	toostotte	gcacccacc	getetttgea	algattgeet	₃ 300
ttagggagaa	acquigaçõe		gaggaagagt	tgcccgtata	taccaagact	360
ccagcgagaa	ggatgeegta	ccgtgtaaag	gaatagaggc	ggtaacgaat	catgacgtca	420
aggetgtgga	gratttcctc	aagagcggtt	cgaggccatg	gggatacgag	atgccaaaga	480
acceat	teggtetgae	ctcgcaggat	gtaaacaata	cggctttccc	gatgatgatc	540
gcgaggcaat	gaccgaggtt	tacttgcccg	ctttacagga	actaataaac	agetteatee	600
ttatgccctt	cagtggaaag	atgtcccgat	act.	3 3 3 - 3 3 3 -	a good a courage	
			9 – –			633

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 577 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...577
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:388

ctcagaaata tccgtctacc atcgtccagt atatcagctc tcaggtagtc cgagtgctca 60 agacatggca aatgcagaag tggagatgca gaaggtacca ccgagatgca acagcaaagc 120 gatgtggaag ctcttgcccg caactatcgg acaagttcgt atctccttct ttcctgactt 180 cggcggaact cgatcgatga acctcggcgt aagcattacc gaatttatca agactgcgac 240 accggcgaag tcaatatccc gatgttggag aataaccact attctttggt aaagtggtgg 300 ctaaaaagtc cggattcgaa tcgctcaatg tggcaatcat tgcctggact ccgccaatct 360 gtctaaggcc gacageettt gcaacgeett gatgagggg gcgaettege tgetgcaget 420 cgcacgttca gcgcagatcc tcctcttgtg agacaggcgg tgtactcacg ttcccccaac 480 cagtttacac aaatgcccgg attagcactt attaccagaa ggctatgggc tcagcagctg 540 cancettega cacetettt ttageggtte categaa 577

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 634 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...634
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:389

gtccacaata acactcgtca aacgatcctg gttggcgtat gatagggaag ttcttccaca gcaatcttgt	tcgagataat caccgggatc ataagccact cgagatagtt tgctacgttg ttgtcggcat cgcacttgct	gaatctcatc gaagccgaac gccaactgta cacccacag atcaccaatt cgacctgagc ttcgtgcggc ccacaacggt	gaaatgatct ccaggatagc ttcatacttg cgcagacagg ccggtttgaa ggttggatcc tggctaacat acctacaccg	agtcaggccg gcttcgtcga catccatgat acttcgaaca ggacgttttt gatctccgtg ccggccccga	caccattgca agccgtatat gccttgcgaa gaggctcgta cgtcgatcct gagccaccag gatttcggac aatacatcgg taatgaggat aagataaaga	60 120 180 240 300 360 420 480 540
ttacccattt	ttatatgatt	ctttgtatga aaaaagattc	ttattactcg	cctgtagcca	aagataaaga	634

- (2) INFORMATION FOR SEQ ID NO:390
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...522
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

gttcgggata gacttcgcac ctcaaagagc gtgatcgtgc catcgccatg	tageggaagt caaactetat tgttecacag egtaegagag gtgggagtat geggtetega	gaccggtatg aaaatgagag ttacccaaac gaagctgctc gtgtccttgc tttcgatagc	teggagteaa aaaatgaaac ageeggeteg ggegegaacg ggtggttgte ttgttcaaga	agaatataga gactcaaaca gcgtgcccat ttctagtatt ccgatctttc	tgacttgtcg aagctccacc agacaaaaag acgcttcgac cgtcgttcgg agactccaag cgcaatccct tggtcatcct	60 120 180 240 300 360 420 480
ggattgttta tcgtcggttt	geggtetega gggeagegat	tttcgatagc	acctctgatc	tteetgteeg	tggtcatcct	

- (2) INFORMATION FOR SEQ ID NO:391
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 674 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...674
- (xi) SEQUENCE DESCRIPTION: SEO ID NO:391

teccegggaa atecetettt teagtatgea acaeteegga aataategeg egatatagtt 60 getettgeee gtteeeteae caccegtaat geagaacaat tgtegtaggt teccaaagga 120 acgtcgttca cggaaataac cgttttgaac gatcgggcgg attgttataa ttgatttcac 180 acgaacttaa aagcatatgg tttgtgtata taattgttcc aaatggtcgg atatcagctt 240 cetgaatett etgtgetgtt teceagettg aagtaategg agatatettt etetgtttgt 300 teceggataa aggeaatteg ateegetgta atttatggtg agaaaacgtt egeaceageg 360 tgtagagget tttatgcccg tttcgtccat atgtacaaaa agaaaatatg cctgaacett 420 cgtgcaagca tttcgatgac gattcttcga tattgcctgt ctcactgttg aaacagatgg 480 catggaatcc tgagaggcaa gggataatac atctttctct cctcccgtga tgaaaagtaa 540 . . tetectettt geggaagttg etecateeeg aacacatagg ttteeggeat atteceeegt 600 aaacgaaccg gcattgactg aaaggacgat atatcttaca tagtctttgc gcaggaagcc 660 gaagatcggc tctt 674

- (2) INFORMATION FOR SEQ ID NO:392
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1338
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392

tctgacttat taaacgaagt gaagtgtagt acttgtggca gctgtttttt ctgatccgac 60 cctactttcg acattgcaca tcacccttgc aggcacatct cataacctgc caacataaaa 120 acacgaaccg gaaacgctcc gactgtgcac gtgttttctg aaaaagtgga accgcaactt 180 tttcgttccg gcacgttttt tttcacttct cgcaccaaaa gaaaaatttt cccacgccac 240 gttttaggag gtagaaatat aaaaaattcg gggcgtaaac tatcagaaca tgggttcgcg 300 agattatece aaaegeatee ttataegate geeteettat ataaataegg agtegtttet 360 atgcagctgc cctatgcaaa atggctatat ttcacgcaca ataaagaaag tcattgcgac 420 aaatgagaac aatcaaactg aagacaaaga gtttgagatt tacattccgg cgactcgcat 480 acatgaagcc ttaagaggat ggctgccgag atcaaacggg atctgcatga ggacaatccc 540 tattcgtctg tatcatgaac ggctcgttta tgtttgcagc cgaactgagc aggctctcga 600

tgagagttat	caagtggatt	tegecegeta	ctccagtatt	gcggtatgca	gagcacattc	660
atactcaaaa	agattatgcc	cataacacca	acatgcgtgg	caggacagtg	gtcatcgtag	720
aagatotgat	taattaaatt	atacgatgag	ttgcgtaaag	gagaatttct	acgagcttgg	ູ 780
aagacccgac	tacacataac	agctatocto	accaaacccq	ctgcactcaa	atggatatcc	840
ayccaayayy	tatacactta	gagategge	atgactttat	cgaggacacg	gccttgacta	900
ataccyatta	agaagatat	accadacat	cataaaataa	aagaatagat	gettaaegta	960
tgatgatety	gyacycacyc	taggggaag	acacccasaa	cgaagaactg	atccgtcgat	1020
ctaatetteg	gracecegg	cccgggaagg	genecedang	cgaagaactg	ctcagaccaa	1080
atggattccg	catatttcaa	eeggagagee	gettegee	gaaatcaaag	agecteated	1140
ctgggccaag	cagcagccgg	ctacatcaac	gagggacacc	tcgtaccgac	tettessess	1200
tggacatgat	ggaaaagctc	atcagcactt	tggtcgtacc	gaggggatta	tettegacgg	
atttccacgt	accattcccc	aagcaaagcc	atggagacga	tgctcgcaca	tcatggatgg	1260
aaggtggaca	tagtctgaat	ctgcaaagta	cccgaggaaa	tgctcatcga	acgectectg	1320
aacgaggaaa						1338
2 22						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 634 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...634
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:393

caaaaaaaac	tgaatctctc	caccaccatt	tccacgagct	gcgtaaaggt	gcaatcaccg	60
cgataaagat	gatcagtgag	aggaagetea	gatccactcg	gcatattggg	atccgagcca	120
adaaadadca	ccaaccttaa	aaatatattc	tqtaacagat	agttgatggg	caaggtgcag	180
accaagatga	aagtcaggca	actccaaatc	cgatagaggt	cttcacattc	ttggaaacgg	240
ccaagacga	cacatteeca	agtagtagge	aaaaaccata	ttgnccacga	atatgagcgg	300
acaaacatac	ttatgtaatc	cataattgat	actotcttaa	ttgttatcag	gegtgteeta	360
cttagttctc	ttgcaaatcc	ttattacaaa	cagatgtacc	cagatgacaa	ctgccacggt	420
astosasacc	atnagagaga	aatcatcaga	ccattattaa	cataacccga	ttcgtagaag	480
gaccagagee	gactttata	tocagoaatg	taccggagcc	cgagcaattc	gcggaagaag	540
cccccgggaa	casascccat	cctatcccag	accoatteea	atccatcggg	aatgacttcc	600
		aaagccttca		333	-	634
aayyacyacc	gggcaaggca	aaagooccoa				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

249	
(iv) ANTI-SENSE: UNKNOWN	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS</pre>	28
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1463</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394	
ggccgtctcg gacagettte etgtteetgg caacggactt tgccaegett gegccgagta gtccgctccg catacttte etttegteet tgtcagaagt tggcgatgtt ttgccgccg cagaaggagagagagagagagagagagagaga	60 120 180 240 300 360 420 463
(2) INFORMATION FOR SEQ ID NO:395	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 451 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE:	
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS	
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1451</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395	
ttggggatte acattaccee tgetgeggte gaagteegta gegtgtacag aaceaegage ggetteeetg taacegttt ggeatgtatg eeggeeggta ggtgageeag tegtgggagt ggateaegte geaeggtatg gtaegegtat eaegeetget aegatggagt aattattgat etetteeage agattgeegg atagegteeg gaaaattega taeageegag ggeateegne tegtgtee aagagttggg teaeeegttt nggtggggae attttgtata etatgggagt eeggaagttgg geetatgagt eggaggaaae tetgteeteg teteeeeaeg gtttgggaat ggaegaaagt aatateeatg tgggetgeat g	60 120 180 240 300 360 420 451

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1036 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1036
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396

+		agggatocca	gtaccactac	agccaaggcg	catctgccag	60
gecaaegete	ggaaaacacg	tastasaat	taggacttca	gcttatcacq	gtcttccacc	120
aaaacgggag	ccatgctgct	teateagger	cagcacccca	gettateacg	gctgtcatca	180
agtatatacc	gggtctgttg	cctgttctgc	eggaeggage	gcgcagtgcc	agggggatt	240
	atceteggea	aaagctgctC	ttcqqaqaac	Lyceyyacay	uguggug	300
++-+-+	ctacaaataa	tttcatataq	acaaaqatac	acaacagco	00009900	360
cttttcatct	acacdadaaa	tagcagcaag	gcagtatgee	ggtttttt	cgcug cu- j-	420
	ccdatddact	ccactcataa	aagactcgat	Cacaaacaag	addadgees	
+++-+astaa	ccasasata	tacacaaaaa	aatttcactt	ttggagteet	ccyaaaaaaa	480
ttettesses	occtcatttt	ttcagaggtc	tatatcqqtt	ttactcgtcg	ccgttcgatg	540
ttattgacaa	~~~~~~~~	agtttccccg	acagecgaea	aaaataattt	tccggccgga	600
ttttctttcc	ggeegggaaa	agecteecy	tocasagett	totacacata	tacgaaagct	660
aaagctctat	ccaaagcctt	cggatatgta	anttagatta	tagettttc	aacttttccg	720
ttgtttatat	atccgaaacc	tttgaaaaag	aaccygacca	tttattact	aacttttccg	780
tactgcagaa	aaaacttttc	cggccgggaa	egattattt	etecaccycc	gtgacctgtg	840
taataataat	acctcccaca	aacqaqtqtt	ccqqtaaagc	accegaceacc	gouaggener	900
	casateettt	cacatetata	cataaacciy	Coggedaded	0000000	960
+ - + +	asaatacsaa	- aatatoottt	acattacaar	gggttagatt	caccecagaa	1020
псававава	tccttataaa	atggngtaca	aagtttttt	gtcgctctgc	ataggtttag	
ccctgagtga		* · ·				1036
ccccyagega	~ 5 ~ 5 ~ ~					

- (2) INFORMATION FOR SEQ ID NO:397
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...643
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397

agccatttca ctgtgtccga	teactteaaa	acagcataca	gcttcgcaag	atgactgcgt	60
testagget catataggets	atacagaact	qaqacaqtga	cagccaaaga	adacyacycc	120
gaagagcagc caaccaaacg	ggcgacttcc	ccacatatcc	aaggtataat	cattcaaggg	180

aagggcagtg tcggggtttg	cagcagccgg	gctttcaggt	ttgagcggat	gcgtgtcggg	240
gataggaggg tttttcagg					300
gcaggagacc caaatcgcgc					360
ccctatgate teeggtacea					420
attteegtee gaagteggee					480
ggttggtaat cgatgagtag					540
gcgtttttat ctgtacgagc					600
ccgtcatgct atccgaatag					643

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2112
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398

cggtcaatgt	gtacgatctg	gggttgatat	acaatgtgga	cgtaggagcg	acgggttcgt	60
taccgtcacc	atgacactga	cggcaccgaa	ttgtcctgag	cagacttcat	catagaggat	120
				aaagatagac		180
aacccgaatg	gaataagaca	tgatgagcga	agaagccatg	ctggagcttg	gattcctcta	240
				atctacttta		300
				agagcgtttg		360
				ggcgacatgt		420
				tcctcgggaa		480
ttgagcgatg	gggggtggag	attcatttct	ttgccggcaa	tcacgacgta	tggctgacaa	540
				ggcattacgt		600
				gtctgtgaag		660
actgcatgta	ccgcctcttc	cgcaatcgtt	ggcacgcctc	ctttatgcag	ccgtgcatcc	720
tcgctggaca	gtcggttggc	ctatggcatt	tcactgaaaa	gcagacgcag	cggagagaag	780
				ctacttcgat		840
				ccgaagtgga		900
ttcggccatc	gacatctgct	ggtcgatatg	gattgcgcga	tgagaagcgt	gtcctgatcc	960
				ggcacgacgc		1020
				ggacagaccg		1080
				tatgggaaga		1140
				atgcggcgaa		1200
				cggccccgaa		1260
				aataacggga		1320
				catggagggc		1380
ccggagctat	tggcttcctg	ctaccgtaca	tegetgteea	tgctttggac	aagggactga	1440
				atcctaaaga		1500
				ccccattgac		1560
				gactgacgcg		1620
				teegeetett		1680
tattcagttc	gctctcaccc	ccccaagggt	tccctccaag	accccttagg	gatcccccct	1740

gagaccccta	aggggtccta	cccggactcc	ttaggggtcc	cataggagac	teeteggggg	1800
tctcaacagg	gaccctaagg	gatcgtcccc	atacttcttg	atgtcttcgg	agaaggtttt	1860
ccaagagact	tttccccctc	ctcctctctg	cacgcttgcc	ctgaatctgt	gtgtcagcgt	1920
cacgtttttt	tttacatttg	tgcctaataa	gctaactctc	aggctaatgg	gaaaattgtt	1980
acaggataaa	ttggctcagt	ataccgagcg	caaaaggcac	aagccgcagg	tatttaccct	2040
tatttcagaa	aaatcgaagt	gatcaggata	ccgaggtcgt	tatcgatggt	cggaaagtcc	2100
tcatgttggc	tc					2112

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 647 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...647
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399

60 gggcgtttaa tcagattgta caactataaa atcangacat cattatgaat ctacagaaaa 120 gaaagaactg tgcccacttc cgtttgaagt tggaaactac ctcaacgagc attttcccga 180 aatgtoggga aacaatocat toattacgca oggtoggatg aagcgotgao tgootactgt 240 gatgccgtgg cacaagcttc tctcatcccg aagccgagag tatggcaagc gaagtcctgt 300 atcaaggetg cattletece gatacgatae cettgtttee gtettggage gggattegag 360 caggaactgc cgtcacctct tcccgaaaga ctcgctccga tacgctaaaa aacaaggcga tacaaagcgt atttgccaag tatgacctta caacgacttt gaggcaagtc cggaatacga 420 480 acatetetae acegaactga eggeacgata gteeteetta tegaaageaa teacetgeet 540 acaataggcg agggaacgat accgtataat cacccaacat cggaagcgtt tcagtatcag agccaagata tgtactccgc ttcacacgac aagggacaag ctcttgtctg tgtcgcgcac 600 647 tatcttgtcc acgctcttga aactctaaaa tgctttgtat ggatata

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...372
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400

cagaaaacac atttagtact agtagtttt tetegateta eccaaggatt gteagatete 60 teeaatgggt ttttaagtat aaaateggaa gggtttatgt ateaagteeg teggeeegat 120 atttacaggt eggaggaett eaeggagete tatteggtat ttegaaegag gagtaceaca 180 teetetacgt ggtggggtgg ggaaacatat ecaeeggaeg ggattttaeg geteggtate 240 tgeeaetgee ateageagg ecaaategeg ggettgtgt geaggattge agetacatag 300 aetateetee tgggtgeage aaagaggttg geategatea eaeetegttg eatgeegget 360 egaggeggat ee 372

- (2) INFORMATION FOR SEQ ID NO:401
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 812 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...812
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

gcgaaaccat tecegaettt catatatgga gtteaggete ggeeaattaa egatgeetta 60 120 aagactgatc cggtgggacg cgctgaggaa gttcgttata catcgatgaa atagaaaagc gagcagagga aatgtgcaag gcggaactct gcatcgtgag ggaaaactgc ccaaacgggt 180 atgccactgc gacacgaggt aaacaacatg cttttcgacg aagacggaca tgtactttgc 240 300 gtcatgacct cgacaccgtg atgccgaact ttattttctc cgactatggc gacttctccg taccggagcc aacaccggcg aagaggacga caaagacctt gacatgtaaa cttcgacatg 360 gaaatettea aggeetttae egaaggatae etaaggggge aagetettte eteaeegaeg 420 480 togaaataga gaatotooog togoogoago actatttooo tatatgoagt gtgtgogott cctgacggac acatcaatgg cgatacgtat tataagatca agtaccccga acacaatctg 540 tacgcactcg tgcacaattc aggctgctac agagtgtaga ggactgcagc tgcagatgca 600 agettttate gaccaatgte ttaggtatta agetettaeg tgtaccaatg teagetaeag 660 acacactttt ctaaagacaa gaagacccac cgactttagt ggctcttcgc acaatccttg 720 cggatacgat gaagcggact taaagtcgct taaccggtca agtttttgat tataaaagtt 780 812 aatctgaaag attatgaact cactacttgc ca

- (2) INFORMATION FOR SEQ ID NO:402
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...524
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402

cggccggagc	tactttcgta	ttggtaaaaa	cggatgtgct	cggacaagtg	atcgtcctct	60
				ctatgttcaa		120
				caaagaactc		180
				tacgatgcca		240
				tcatgaacgc		300
				cgttgcagct		360
				gettetetet		420
				aattcgaagc		480
			tgcccgattt			524

- (2) INFORMATION FOR SEQ ID NO:403
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 535 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...535
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:403

ggtcgatacg	ttcttttagt	ttggcgtgag	caatatcacg	ccccacgata	togtaccact	60
			cgacagcttc			120
			ctgtaccctc			180
			ccagataccg			240
			atacctacgg			300
			agtatttgcc			360
			ttcagttcga			420
ccttcgtttg	cccgaagtag	gagattgtcg	taagtacttg	gcccgaagcc	agctttgacg	480
			ccgcctattc			535

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 865 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...865
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:404

60 gtgccatcat ggctgtgctc atcggactgg gttatacacc gagtgagata aagagataat 120 gtggtgcctc aatttcaaag aatttcatgg acgattcggg ggtatcattc aagatacgaa acgggcttga tcgagaagtt cggttggaca aaggcgattt cttccgcaat tggcttggcg 180 240 acctgatcaa ggccaaaccg gcaacagcga atcgaccttt gcggatttgg ctgcaatgaa 300 aggagaaaca aatttctcga catttctctc atcggcacca atctttctac aggctctcag 360 agatetttte ggeagaacat acacetegea tetgtatage egagetgete gtatetetat 420 gtccattccg ctgtttttcg ctgctaagcg cacttccgaa acgatgtata tgtggacggc ggtatgctga acaactatcc ctcaaggtgt ttgatcgtac caagtatgta accaagaact 480 540 ttacacgaac ggctactatg aacctatcaa taagaagctg gagaaacgcc ccaggaagat 600 gccgattacg tatacaacaa agaaacattg ggcttccgac tcgacagcaa gagaagatag 660 ccttcttcag ggacaacgca gaacctcctc atcgagaatc gacagcttct ttgactatac cgtgtcgcta ttcggcactc tgctcttgct caagacgatg tacacctgca cagtgatgac 720 780 tggcaacgca ccattacatc gatacgctgg gagtaaagac tacggatttt gccatcagcg 840 atgccaaaaa aaagctttgc tggaatccgg ccgctcatac actcagtcat attggagtgg 865 tacaataaca gcgaagaaaa agtca

- (2) INFORMATION FOR SEQ ID NO:405
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...488
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:405

gtttgaggcc	gatatggatt	gttgcacggt	gcgtctacct	gtcggtgacg	ttataggcct	120
			cttgctgata			180
ttaatttgtc	aaaatttaat	gctatgcgga	caaagatata	taaaaaaccg	attggcgaac	, 240
tctgaaatta	agtcctccaa	tcggttttgt	aaattgctaa	aaagcaacaa	taatttaatg	300
agtcttttt	gactctcttt	tttattgctt	atcagttgcc	tttcgtgctt	cttggcgtgc	360
gggcaatttc	ctgcttcagc	tttgcctttg	cctcgcaaga	tttgtggccg	tgcttgctct	420
			actttttttg			480
gctacaat					-	488

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...534
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:406

ggagtccgcc	cccttccttg	gcgatgacga	acggctcttc	tggcagaggc	ggaagatcgg	60
			ctcggcttgc			120
			aagcggtata			180
cttcacttgt						240
acggcggcgg	ggtttatctc	cgggcgagct	gatgatcgat	gaagatcaga	ttctctcctg	300
agagagacgg	atcgtttcga	cgatttcggc	agcagtggct	tcccttctac	ctgctcgcgg	360
			attctccggc			420
cagcctcgat	catttcggtc	atttgcactc	gtgttcgtac	acctgttgga	atacctccaa	480
tacagagccc	aacttctggg	gcacggcatc	gatagettet	atcttcacct	cqcc	534

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 632 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

gttcgaggta	gcagaggtag	tgtcccggca	cgcagtgcat	caggaagaag	taaggccgaa	60
gatcagcacc						120
ccgaatatgg						180
cgattcctat						240
gctcatgccg						300
gtgtacgtgc						360
tactatcggg						420
aggatcagca						480
cgcggatcag						540
ggtgtaagct	gtttttcttc	catttttttg	ctatcccgtt	agtggttcta	ttccattttg	600
aaaatgtctt	ccgcaaggca	tttcttaccg	ct			632

(2) INFORMATION FOR SEQ ID NO:408

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:408

tggtttttgt	ggaagatacc	ctgaagcgag	aaaagaaaac	cgaggcgcat	gtgtgttgga	60
			tttgtatcgt			120
			tggagctatt			180
			gaaagggtat			240
			gagtatgaat			300
			tggaatacac			360
ccacagcgga	cgggattata	cggcttggta	taccgaggat	attgccctct	cggatgggcn	420
cgtacatttt	tcggggattg	ccggccttga	ttgtggccat	cgcttcngat	gatggggaat	480
atgcattcca	cttaatggaa	tgcangggga	gattactttc	ccctcaccta	tatttctgtc	540
cacaaaaag						549

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...533
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

gcctatcttg	ttgcagccat	agttttcttt	tcggactatt	ccgatagcat	cgctgctcag	60
gtttggaagt	tcgagtcgag	ggtaagacga	aacatgcatc	atgcaaaaga	ccgatgtgga	120
gcgagacttg	aagcgtctgg	gtttcacccc	tatggcaagc	tgctcgactc	tatcgatctt	180
cacagaatgg	aaagaacctt	cgtgctaatt	cccttttccg	cggagcggaa	ttgtatgcct	240
ctccaccggc	caactgtatc	tgacagtgga	acaaaaagat	ccgctcttta	tggtgtacga	300
teegataeet	ctttctatgt	ttctaccgac	aggagcgtga	tcgtcccaac	ttgcagtatg	360
ctgcccccgt	actgatggcc	tcaggggata	tactctgtcc	ttagctaccg	gccctctctt	420
cgacctcatt	gcatttatca	acgatgatcc	attctggnca	aactttttcg	ctcaaggtta	480
tgtgcccgga	aatggncaga	acatattaag	ttccccgtct	gggcnaaact	gga	533

- (2) INFORMATION FOR SEQ ID NO:410
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...493
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

acgaatacct	ctgctccgcg	atagatgccc	ggcaggaaag	caaatgggaa	tcgtgcagca	60
		cctgatcgct				120
cgtacgcttc	cctacggcga	cgagccgata	tgtcggtcac	ggcaatgtgc	caaagcctcc	180
acggccagtc	ggaggtcttc	ctcgtctcga	tgcttcccac	atagagcagg	taacgctcag	240
gcaaacatat	cgctccctcg	ctctcgactc	atcctcctcg	gtagcctgtc	cgaagccggc	300
gaacaaccct	gatagacgac	atcgatccga	teggeaggea	cgtgaaaaac	tccatcacat	360
		atcgctatca				420
		ctgtccacag				480
tcaagtcgtg	atc					493

- (2) INFORMATION FOR SEQ ID NO:411
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...577
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:411

ctttttacgg ccttttttgc tgtcggcaaa gttgtcgaaa gcgaagatcc tttccagtcc 60 120 teggeattgt cettgactgt ggtteggeet eeetgetttt eaggtgeagg tegtegtaeg ggcgattgtc gaaggtggtg gagcggtgcg gatctctccc tgcgtgacgt ggatggtctg 180 atagaggtag aggccgagcc gatcctgtcg tgctgctcgg agaatccgtt gcggtagtgc 240 300 ttqqqqatqc qctqctqatq atatatacqq qtqtcqtctt cgtgccggac tccgcttggt ggtgatacgg gagtaggcat gatcgtgtcc ttgcaggacg aggcggcacc gccttcctcc 360 420 agaatggagc ggaagccgta gcggatgatc ggttcatgcg tccctgccgc accgaataca 480 ctccqtqqtq qaacatgacc acttccacgg ctgtacggtg gtttcgagtg cgtttttcaa 540 ccacqtqcqq qqttqaatac ggatqccqqc cattqqatqt ccqtqqtqtc catqacqata 577 accegcatat gggggaagte tatgtagtac gaacgcc

- (2) INFORMATION FOR SEQ ID NO:412
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 668 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...668
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:412

tgccgagaaa tctcgggtc	g ctgtacgctt	tcaagttcag	ccaattcggc	aaaattttat	60
cgtaccette etgtgtaat	a taattgtatg	ccatactgct	tgtatgtaac	gttggttgaa	120
aaaaaaattt ttcttcggg	tgcacctaca	gccattctcg	tccaaagaga	aaaaagaagc	180
ccggaagata cccataata	ggaatgtctc	cggaactctc	tactctttct	ttaagtcgtt	240
tgagcacttt acgctcggt	g caaagatagt	aatctttctt	ataagagcga	ctttgttctt	300
cggacgacca gggtgcaaa	tccagcaata	agtgcaacac	tatgtgaatt	ctgtaagaag	360
cactegaacg gagtgccga	tccgagtttc	ttccgggtct	gtggttcagt	ttattctgta	420

taatgagacc t	tttgcacggc	attggcgtgc	aaaggtctct	tttcaggtgt	atttgaggga	480
aaaaaattga g	ggctccagcc	ggttctccat	cagcttttac	ctccaccact	gtttcttttg	540
agcaaaaaga a						, 600
gtanggcgag a	acggtgcant	cgaccaccgt	ggtctgtcga	acgggatgat	tcctccgcga	660
gtaccatt						668

- (2) INFORMATION FOR SEQ ID NO:413
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 609 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...609
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

cgaactgctt	ttgcccacgc	agcgaggctg	ctnagggtgc	tgnagacggc	gagttcatcc	60
ccgtaggagc	cagccagtcg	cagaagacgg	atgtccgttc	gtagcggcga	cgaatgtgaa	120
cctcaagnag	gcggtagcga	acgggaattc	cgggaagacc	tettetteeg	gctcaatacg	180
gtaccgatcg	aggtgctgcg	ctgcgtatgc	gaccggacga	cgtgcccttg	ctttttcgcc	240
gattcccgcc	gacagcgccg	agaagtatcg	gatgcctccg	ctgcgcctat	cggagaagcc	300
cgtaccatat	taatgcgtta	ccgctggccc	ggcaatgtgc	gaggctgcgc	aatataaccg	360
acaggctgag	catcctggag	gaggagcgga	cgtatcggca	gagaccatca	ctcgctacct	420
ggacgctgag	gggatgcaag	actccacccc	gtcgtgatcc	gacggaacga	aacgaccgaa	480
gcggacaaac	aatcccccat	tacgagcgcg	aaatcatcta	ccaggtgcta	tacgatatga	540
gaaagagata	gccgatttga	aggggatgat	gaaccgcctg	gcgcaccaga	acagccctca	600
tggcctgta						609

- (2) INFORMATION FOR SEQ ID NO:414
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414

ggctacgatc	ggtagcgtgg	gcaactctga	ccatgctctg	gaaaaatcgg	aaaggccggt	60
cgttctcgct	ggttgggtcg	cagacctcac	aaccgagggt	ggtgatgaac	cctgtggatc	120
accccatggg	tggtggtgaa	ggtcgccgtc	aggaggtcat	ccccgttcac	gcaagggctt	180
gtatgctaag	ggcttgagac	aagagctccg	aagaagcatt	cttctaagta	catcattgag	240
agaagaaaaa	gtaatctgat	ttaatcaaag	aaaattatga	gtcgttcact	taagaaggtc	300
catatattaa	tctcaagctg	gaaaagaagg	tcttggcgat	gaagagagcg	gcaagaaagc	360
tgtcattaag	acgtgggctc	gtgcctcaat	gattctcccg	acttcgtggg	acataccatt	420
gcagtgcata	acggaaataa	atttattcct	ggttttggta	cccgaaaaca	tggtggggca	480
taagttaggg	aagttctttt	ctacacgtac	ttttc			515

(2) INFORMATION FOR SEQ ID NO:415

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 853 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415

ggcgcagttg tcgggtaate	ctttaanaca	tttcaggaag	cgattccgga	aggttcctcc	60
gaaggcgatt ccggcggtg	, aaacaccaac	ggagcattac	gaaacaacct	aaaacaacga	120
acagctaaca ccttacttta	ı tggaattaaa	tcattgaaaa	atatcgaaac	atcgttccgg	180
cagateegge tttatgeatt	geetttgteg	tactctgcct	cattatcacg	ggctatgccg	240
tttttcatcc tattcctttq	, cagaaaaaca	gcgggagaaa	gtctatgtgc	tggaaacgga	300
aagtegetta tgetegetet	cagccaggat	gccaaagcca	acctcccgtg	gaagcccgcg	360
agcacgtcag gcgttttcac	gaactcttct	ttcgattgcg	ccggacaagg	cggccatcga	420
agggaatgtc aaacgcgctt	tatgctggcc	gacaaaacgg	cctacaatta	ctacaaagac	480
ctgatggaaa aggatattad	agccggatga	tttcaggcaa	tatccaccag	cgtatcgagt	540
cgactccatc cggtgcgatt	tegaggeeta	tccttatcgg	gtcaggacta	cgcccggcag	600
tttatcgtcc gccagagcaa	catcacggag	cggtcgctat	caccgaatgc	agcctgatca	660
attccgttcg ttcggacaac	aatccgaggg	tttcctgttg	gaacgtttta	ccgtgctgca	720
aaatcaggac attcaaccgt	gaaacgantg	aaacggttct	atctgaaaat	acacctcggc	780
ctaagcggca atgtgaccgt	ttaagccccc	tgcaacgaaa	aatcgcggta	ttcggctgag	840
cctgatttat ctg					853

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 410 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...410
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416

ggtgatacgc gtattctccg	taacgcgctt	cataaagagc	aggatggcca	aagcagtcct	60
atctctatgg caacggtcas					120
ggetateget gegagggeeg					180
ggatactatg atcagtctcc					240
aggaaagcag gatcagcagt					300
googttgttg atgttggtos					360
aacggaacca ctatattgg					410

- (2) INFORMATION FOR SEQ ID NO:417
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 568 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...568
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:417

gtgtagggcg cacaccggat cgctatggta ctctctatcg gtctgccggc ggtagaagcc gcaggcgaaa	taaggcactg cagggtgcgc tgcagaggaa aaggcttgca ttcttccgat actgtgtctg gtcggatcgt	gccgatgatt actttgcctg gcgatcgagc gatgtggctc gcgatatatg tccgggctcc tcggtggaag	gatatgccgc tcctccgtct ccttcaggcg cttcgctcgt ctcaatcaga ctctcttgtt tgacctgcct atctccgca ttccttcttg	atccgtgagc gatattattg atcggtacgt aaagaactca agggcaggaa tgtcaggtac aggcaaacta	atatcateeg gtgegaeegt etcaggaeag gettggeega aagategaat atttgeeggt agtgeagage	60 120 180 240 300 360 420 480 540
	ggaaaaggat	ttgcttgggc	ttccttcttg			540 568

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 562 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...562
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418

ttcggaggtg atcaagtgtt cttttgtcgg tgaggcagag aaaatcgcaa gctggaggtc 60 gtgatgcggc gcgactatgg agacaaattg aatatattcg ctcttctgaa acgctgcttg 120 agtgccttcc gtccgaggtg cagaagaaaa agccatatcc gacctcttgg acaagctgga 180 tttgtcacga gaggaattgt ttcggtcgga gacagctact gcgatgtgga gatgatccaa 240 ctgggcggct tgggtgtggc ccgtggcgaa tgctcgggaa gccgtcaaag cctggccgac 300 tatattacga cgagcaacga ggagaacggt gtcgcccact tggggacaag tatatccgac 360 acgaatatga agccgttcct ttctccgtag aaatgtcaat agtattgtgc cgggtacgct 420 catggagage cttggtatte gtgcaccaag ateegegegt ggetatgteg aggeaacgat 480 geeggtggat ttegeacteg teageetatg ggtattttge atggaggage eagettgget 540 ttgcagagac cctggccggg at 562

- (2) INFORMATION FOR SEQ ID NO:419
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 788 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...788
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

gacgaagtcg tccc	atacca tacccgaccc	tacacgcaaa	agaatgctgc	ctgatccttg	60
tgcagttcgg ggata	accett tactteggaa	tgaagcagat	accatgaaaa	ttagcgagga	120
agagcagatt gctco	eccteg ceaatagttg	tacgcgacaa	tcttgaaaga	attcgtcttt	180
caccaaccga tcaat	acggc gtcgcatgtg	tagtcaatcc	accaatctgt	ccgggctgca	240
ataccaatgt attgo	gcttg gagagtggat	agtcttgtct	gatgtccatt	agttgcacgc	300
tcaagcagcc atgca	atcctg aaaattcgga	gcatagcgtt	cctgacggcc	tcacgggcag	360

ttctgccaaa gttgcattgc actgtaagca ggacgagttt	ataggggtat gaagetgeet gagagetttt ccatateett gtaggeactt	accttcagat accactacac cttgacggat gtcttcagct tgcttgattt	tccaagcgtt tgaaccgatc ttgtacattg tgggcaactc gcatgagccg	cattcagaga caatcgagaa gtagccggtt acgttctttg aatgcaaccg	gcatettece agaaactate gcctgctcgt tcatagctat	420 480 540 600 660 720 780
aagcttggcg ggcggctgcc atgccaaa	gtaggcactt aaaacaccat	tgcttgattt cttattcatc	gcatgagccg tgttattctg	aatgcaaccg gttgagttat	taatactccc	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1055 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1055
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420

```
60
agtcggagtc tggacacggt ccgatggaaa agtacctgtc gggttgcccc gaagcggaag
                                                                       120
cggtataaag acgcgtagcg ttcataccca atagccagcg cctatggcac gagccagtcc
ggcctcatat agggaatgaa attetteetg tegegeagee tegeaaagee tteaeggata
                                                                       180
gacteeteag taagagagat atecaaagte geegeaeggg acatgtgeag eeegtttet
                                                                       240
                                                                       300
gcaatcccaa cgctggatca gctctccctc ctgtccggca tcaccgcagt tcacaccata
                                                                       360
tecgetteat ggacaageet ttegatggtg cegaattget eccaataeta tegetatega
                                                                       420
tgagtttgat gccaaatcgc agtggtatca tcgtagagaa ctgatactcc atcgcttcca
                                                                       480
ttcgggtgca tagtcgtgag gtctttgagg gcacagagat gtccgaaagt ccatgtcacc
                                                                       540
tgataaccgt gccctccata tagcctttat aggctttggt ggcaccgagt acagcagcgt
                                                                       600
ctcacgcccc acactgggct tttcggcaat acagactatc atgggctttc cttgattctt
                                                                       660
aaaaacaaat gtacactttt ggccattacc cactgtgctt gattgaaact attaatcggc
                                                                       720
catttgcttt tcacagattt gtcattgact ttttcacgga cctttgattt atttagctct
tocccatagt gotaaaatgo aattotatgo ttoagagooa gagooaactt cagagtttto
                                                                       780
                                                                       840
ttgctacgtg tttttggatg taaataggtt agctaaaaac ttcattcgga ttgttngaac
                                                                       900
tngggcttct tcacagagtt gatttaagat ttagtcgcat aacttatatc gaactcacgt
                                                                       960
tataagaata acgcgcagca agggggagga aggaaggaag gaaaaggaga aagaggaata
                                                                      1020
gagagaaaag caaaatgatt ttggagagag agaaaataaa aaaggagaga gcctcggatt
                                                                      1055
cgagactctt ccttaccttt ttttccgggg aggag
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:421

tgaaaaatct	cacgccacaa	agttttcatt	ttggtttgaa	aatttttcct	tccgacgcag	60
gaaaaaaata	ttttacgcgc	gactttttga	gtcctcttag	taaggtattt	tttttaacat	120
acttgtaccg	aattatgcat	ctaaccaagt	gtagaatcct	catctgtagg	taatttqcac	180
cgaacaaccg	atttgtagta	cattatgtct	gacgaaacgc	gtaattttga	cttcaaatga	240
aagaagattg	aaccaaaccg	tacgctattt	tctgcctata	ctcttcgcag	tatageegge	300
ctggtcatat	ctttcactca	cgtccatatc	atcaatggcg	tgacatcgtc	cactcccacq	360
tacagtgggg	cgacaacgaa	agcgatccgc	agacaatccg	cattcggatt	cggaattgat	420
tctgtacaat	cagctttcgg	catattcacg	acttatttgg	atacgccggc	catagacttg	480
aaagaacctg	gagggttgtc	ggcgtcgttc	ctttcttttg	cgataatctt	actgctctct	540
ttcggagcta	actectteca	atcatctcag	ggataa			576

- (2) INFORMATION FOR SEQ ID NO:422
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 619 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...619
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:422

caatagaaag	ttggcagaag	agaatccccg	acgctggcag	cacttnttca	ggacgattca	60
cccnctgctc	cggcagcatt	ggcttatacg	ggtatggttt	caagaagctt	gctcctgcca	120
atttcaatgc	tgacgattgg	ctctatgctc	cgaacatctt	cttatcacct	cqttcctcta	180
cggtcttttg	cgaccggtga	catgattcgt	ccatacagga	tggaaggatt	tgcccatctg	240
ggggccccgt	cgaagatgaa	gtattcaact	tctggcgacc	gtatcttacg	gatttctgat	300
cgaaaaggta	cgagaaaagg	gtggtgagct	atgttttctg	gccgtgaaga	aatgaaaatg	360
ctattcgact	ggaaacgagt	agaacaagcc	gtcgggtagt	gacacccctc	ttcaaagtac	420
cacagecega	tggaggtctc	aacagatcgt	gatctatacc	aaaatggcac	geggaetgat	480
gacagcccac	tcctcacccg	ccgatgccgc	catgtggaag	agatgcaact	cttttcgccg	540
aaggttttat	cttccggccg	gagctttcgg	atgagagcaa	ctatctttcg	tcatggaatg	600
aatcggtttt	tacgaccaa			_		619

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 653 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...653
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:423

gcgaagaaga gcaacgttgg	cacaacaccc	atcctgattt	ggcagccaat	tcgatgcgtg	60
gtttgccggt caaacgcccc	aaatcdactd	gaaagctaag	agcagaaacc	caatcaggct	120
geergeegge caaacgeeee	agtattaata	ctcttaccaa	agaagtggag	aatatgattg	180
accegeteeg ettetgeeae	cytyttygta	cccccgccgg	ttattaaaa	aaacccacgc	240
taacctctgc cgaccttcca	attcagacaa	gaeegaegge	-t-t-t-aaga	actaccataa	300
catgagaaag gagatttcag	tggagcattc	ctgcagatgg	gegeategga	geegeeaegg	360
cctgcctctg tatcggtatg	gctcttcatg	gaggcgtcat	teegettgeg	gtacettett	
cgtattttcc gactacatga	aaccggccgt	tctatggctg	ccctgatgga	attgeeegte	420
aagtttatct ggacgcacga	tctttccgtg	tgggcgagga	tggtcctact	cacgaaccgg	480
tggaacagga gcgcaaattc	gcctgatgga	qaaqctqcac	aatcacagcg	gccgtngctc	540
atgctggtcc ttcgtncggc	cgatgtgcaa	gagactaccg	tagcttggag	atggctatgg	600
agaatacgca tactcctaca	actotaatoo	tttcgcgcag	aatatcaccq	atc	653
agaatacgca tactcctaca	getetgatet				

- (2) INFORMATION FOR SEQ ID NO:424
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 947 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...947
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424

tcacgcattt cgtttttttt	ttatttaatt	aagtgaatta	tggtgattat	ctcgnnttgt	60
tettttett gagecatgae	gatgtgcaac	cacadadaaa	tctcccggga	ggtaccacga	120
aggccgaaag gcttgagatt	tassaggass	atacctccca	atacqaaqcq	tggggaggta	180
aggeegaaag geeegagaee	cguugggguu	augustaary	, , ,		

gggg ttatactata	aagggtggag	gcttttaaag	tataaagtgc	240
aggt cttcggcggt	tttattceaa	tacaasass	actatagege	
	cccgcccagg	cycygacaaa	egteteeega	300
gata tgagtgggca	aaaccgatac	gctcgagact	tcccgatgga	, 360
taac aggctgtttg	tegeetttta	caaatgtaaa	taggggaggg	420
cggc atccgacago	tgctacgggg	ctatcgtcag	tagtaaggat	480
ggaa aaagcgcaaa	gaacgacttg	gtatgcagtc	qtccqcqaaq	540
tatg tcccgataca	tagttcccga	tgataaatta	attgagagag	600
stat attcagagga	tagaagttt	++	**************************************	
acae acceagacya	cegaaetttt	tteegaeetg	tataagatta	660
yaaa cgcttgaaca	cccggtggat	aaagaggggc	atgaagtttc	720
aag agcttcaggg	cgatggcggc	acaggettet	gcatctgcca	780
cca atgtgtatcc	acancattan	actecaataa	7777777	
	acageaeegg	gecacggegg	gcaacgatga	840
irra deddedtdet	gcctggagcg	tgagaagaat	gggtagtcgg	900
atc ctgaataccg	cttgaggcaa	ccttcgt		947
	aggt cttcggcggt gata tgagtgggca taac aggctgtttg cggc atccgacagc ggaa aaagcgcaaa tatg tcccgataca atat attcagacga gaaa cgcttgaaca caag agcttcaggg gcca atgtgtatcc gttg gcggcgtgct	gata tgagtgggat tttgttcagggata tgagtggga aaaccgatactaac aggctgtttg tcgcctttta cggc atccgacagc tgctacgggggaa aaagcgcaaa gaacgacttg tcccgataca tggttcccgaatat attcagacga tcgaacttttgaaa cgcttgaaca cccggtggat caag agcttcaggg cgatggcggc atgggggtgttg gcgagggggtt	aggit cttcggcggt tttgttcagg tgcggacaaa gata tgagtgggca aaaccgatac gctcgagact taac aggctgtttg tcgcctttta caaatgtaaa cggc atccgacagc tgctacgggg ctatcgtcag ggaa aaagcgcaaa gaacgacttg gtatgcagtcatg tcccgataca tggttcccga tgataaatta atta	gggg ttatactata aagggtggag gcttttaaag tataaagtgcaggt cttcggggt tttgttcagg tgcggacaaa cgtctcccgagata tgagtgggc aaaccgatac gctcgagact tcccgatggacaa aggctgtttg tcgcctttta caaatgtaaa taggggaggg atccgacagc tgctacgggg ctatcgtcag tagtaaggat ggaa aaagcgcaaa gaacgacttg gtatgcagtc gtccgcgaag tcccgataca tggttcccga tgataaatta attgagagag atat atcagacga tcgaactttt ttccgacctg tataagatta agaa cgcttgaaca cccggtggat aaagaggggc atgaagttcaag agcttcaggg cgatggcggc acaggcttct gcatcgcaagttg gcgaacgatga gcgatgtgtg gcggcgtgct gcctggagcg tgagaagaat gggtagtcgg ctgaataccg cttgaggcaa ccttcgt

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...352
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425

ggctacaato	tgagcgaaga	gacgggaatg	gtggattacg	accacatggg	aaaatggcca	60
tegageacaa	a acccaagctg	atcatcggcg	gtggttcgcc	tattctcgtg	agtgggacta	120
caagcgtat	g cgtgagatcg	ctgacaagtg	ggtgccttgt	tgatgatcga	tatggcacac	180
cctgccggtd	tgatcgtgcc	ggtctgctgg	agaaccccgt	gaagtatgct	catatogtta	240
cttctcgact	cacaagacac	tgngtggccc	ccgtggcggt	atcatcctta	tgggaaggac	300
ttcgacaato	nttggggcaa	gaaaaccccg	angggcgaga	tcagaagatg	ag	352

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 523 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...523
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426

60 cggcgatttc ctaaatatac gataaattat agagtttttc tacatagttt catttaatag ccagtgccta aaattctggt aagttttttt tgtgttggaa gcacttttgt attaaaaatt 120 aaagcaattt ctccatcagg acaaaaccaa tggatttatg tagaaatggt aaaaccatct 180 ctttgccaaa attatattga cacaatagtc cattatcgat tttgacaatt tcttagtccc 240 aaaagtgggt toccaataac caaattcaco ttttcaaaat catcaggatt cactocccaa 300 360 tagtateceg acaccacaga tttttteett tttttettt aatgaaatat egttaggatt 420 atctatcaaa taagggaatt tattggtttt gttatccaga gtttcttggg gttaagatgc 480 tcaactaatg ccaaatatag gtgaaagctg ttactttaat agctaatgga tctatttcga 523 ttccaaagat tttttttacc aagtatatca ttaagttctt tga

- (2) INFORMATION FOR SEQ ID NO:427
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...473
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:427

ggattctgtg	cattacatqt	ccgtggtaaa	gcggtttgtg	cctgcgataa	attcactgcc	60
ttcaggccgg	atagccaagc	ggtcggctac	qqccgagaac	ttcctttggg	cagggtaaaa	120
ggtaagccag	aagagggatg	atctgtcttt	tttqtctcgc	ggatatgacc	ggacttcccc	180
agcagtacat	atcogatcto	tcttattctc	gtccaaggaa	gcaagagcta	aatgtataag	240
atctccacgg	tagagaggga	ttcgggcttt	tqqqaaqqat	gtaaccacag	atgctctcgt	300
cettegeteg	tateatagee	acataaaqaa	gattgaggtt	gtcaggagaa	tatoggotot	360
ttctcggaaa	taatctgtgg	caaacattqt	tttqccatct	ccttcttata	tctgatcggc	420
actnacgggc	aggatattga	aggactgcgg	gcaggatcga	tcttgcacca	gaa	473

- (2) INFORMATION FOR SEQ ID NO:428
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO

269

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1262
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:428

cgggccaage ccgaggagee gaacatetee teacetteet cetgaegege agateeaceg 60 aagtettgat caegttgtga geettetteg atgtaatege geatatacea ttaegatace 120 ggcagccacg aggaaatata cgggagtgaa gccggttcgt tcaaggctcc catcagataa 180 gtatcgtact geoegtteeg ttggeattga agtecanata agaggaataa ceggneageg 240 gcacacgata aagttcacca agtcgttgcc ggcaaaagcc atcgccaaag cgaagtaccc 300 aagaggacga tcaccttgaa gacattgacc cgtagccaat acacacctgc atcaggataa 360 tggaaacgac cagacagtac aataccagcc tgccgtattg gcagctatcc aagccgtgga 420 ttcttcggtc ataaaggaca cccttcagc cctttgatga gcatgaaata aatgatggat 480 gtaaccgcaa tccgccgaaa aggccggcca gccatcggag attccgcctg taattaaagt 540 aaagagcaaa cggctcagat actgaacgac catcccgaag aagaaagcat tcccaccgaa 600 aggaagatac ccaatatgac ggaaagact ttctccgatt gagaagatcc tgaaagccga 660 ccgtaccgcc caccttggtc atggcctaaa aaaagaaccg cctaacagct cgaaaatgag 720 cgagacggtc gtagagtagg catgccgagc gaattgaaca tatccatcag gacgacatcg 780 gtgacaccac cgacagaaat acgaccatca attcgctgaa agtgtaatgt tccgcctgaa 840 aatcccgtgt cgggcgatct ccatcatgcc gttgttcatg gcgcgccaca aaaaaccccc 900 aacgetgeea caeegaegat gatettgaat gageageett ggeteegatg geagaattga 960 ggaagttgac cgcatcgttg tgacacccac aatcaagtcg aatatagcaa ggatgaaaag 1020 aaatacgaca tggcggtaaa gataagactc cattaaatct atgttatgag gttagactca 1080 caaaaaaatt cggcgaatac ctttctctct ctgtctcccg gcaacgatcg gactctcaac 1140 tgggcaagag caaggttcgc ctatccgaca catcttcttt gcacacacaa aaatagcgca 1200 attettaaga acgcaaaaag ceegtaeggt ggtetteeeg eettgteaga teeeggettt 1260 gt 1262

- (2) INFORMATION FOR SEQ ID NO:429
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1208
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:429

cgcttttact cgcatcatga aatataaatt ctttatattt gcgttgtttg aaaatgctaa 60 ggtacgatat tttgattgtt atttaatgg gatcgtacaa gggtaatcta aatagcaaaa 120 tgatttgtca agataagagc aactaaagac taataatata gggcaagaaa taatgcccgc 180 ggataagtet gacagaggaa atcagtaget aaggteatta tteetetege eataggeggt 240 ctgctcttct gggtgggtgt accgcaaaat ggatttctcc gccattggca agatgtccgc 300 , 360 gacggtgtca attactacat catagctttc tetetettgt tegattggcc gccaactgta tacgcggcct gcgctggcaa ctcctcatag aactttggct tctcctcatc cacggaaaat 420 caatgecatt etgactaett tggcaattae aeggteaata tggetetgee eegtgeegga 480 gaattttggc atgcgcggaa gaaagccgct acgagaaaat acctttcccc caactnetcg 540 tacgcttttt atggacagga tcatggactt ggtgatggtc ggacttatac attgagtatc 600 atgatgggct ttcaagggtt tttctccgct tttttcgtcg caatccacaa ctgacacaag 660 getttttcae cattttcagt tecategget atacgttgtt gttgtaggta tegggetaet 720 tttcttcttg ctctaaaata cctctcacac gtaggcccca ttcgcaaagt agcagcactc 780 atcgtaggat actggagggg cttcggtcta tctggcatat ggagcacaag tggtcttcat 840 cttatattcc atcctcttgt gggtaggata tttcttttac tttacaccac attctttgct 900 ttegaettta caegategtt ggggatggga gggggttgat cagettegee atgageagea 960 tagccgtagc cgtacccgta aggggggcgt agggccgtgg cacttcatgg ttattgctac 1020 tettgtgget teggegtgae gaaagaagat geeggagegt ttgeettggt ggtacacaga 1080 ctcaaaccgt ttggactacg gccgccgngt tcgtggctat cggcttgttc cttttgtcaa 1140 taagaaatac gatcgcataa aacagtcaaa caattacaac aatcatccaa aacacttttc 1200 1208 acagtatg

(2) INFORMATION FOR SEQ ID NO:430

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...305
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430

ttgcttcaat gcttcatatt tatttgtcat ctgcatcaac ggagcctggg gaatgcctta atgaaggtct atttcacgat tataagtctg attgagcaag	acttgacatc cgaagtcctt gagtactgtc	accatagggc gagaattgat ccctcggact	gtgagaegta gettgeagge tgagagetga	gagggtgtag atcagattga	120 180 240 300 305
qcqtt					303

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...652
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

cgcggctctg cctgtagagt ctgtacgctg aagtcaacga agtattccaa ccggcagtcg 60 geeteageee gtetaegggt acaataatgt eegatgaate tgaggatega tatetaagee 120 gatgacettg ctttgcaatg ctttgcctta geegaaaceg tatagegeag geggtattte 180 ttgaggttgg tgaagtgaac cgattcgtga tacggaaatg tcccttggcg gcatccactg 240 cttcgagccg acgttttgat gcacatactt cacctcctgc atggcagggt gagggtgcgg 300 tegggattga ecagteegtt geaaaggaag ttgeegteae tegtgeatee acteegaagt 360 ctcctccata agcccaatag gactttcctt tacgtctgta cggaggatac cctgatccac 420 ccagtcccag atgaagccgc ctgcaggttg gggtacttgt agatagcctg ccactgcccc 480 cataggttgc ggtcgaattg cccatggcgt gagcgtattc cgaagggatc acagggcggc 540 gctaccggcc cgtccgatac cttccaacca tttcgcatcg ggatattggg tacatacata 600 teeggattee acteceatty ggeacyttey tagtteacyg gegegeeate ag 652

- (2) INFORMATION FOR SEQ ID NO:432
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 868 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...868
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:432

gateceeteg geatacagta geagecaaca ataccaatga ggagaaaceg etegaatgaa 60 accycaaaac caatttaaty cytcyycece gygygcayet ytcagygcya tegeytttya 120 aaatttttag tototttoot otatgattga atototggca tatggattog cacttgtttt 180 gataattgaa tgtagcatcg ttaggtttat aagtgtgttg acagttcaaa tgcgattgcc 240 ctgtaccgag aaataatgca gcaactatct ctcggaaaaa gcactacctt tgtatcattc 300 caatttaatt acgtagtaat caagcagcaa attgcgtgtg atgaaaaggt tatccgcaga 360 gctctcatat cggtctatca taaagaaggt ttgccgagat actggccgaa ttgaacagac 420 aaggggtaga gttcgtatcc aaggaggaac tcatgaattt atcacttcgc tcggttatgc 480 gtgtcgggcc tggatgatct gacgcgttat cettcgatgc tcgggggacg ggtgaagact 540 tacacccaat gatettegge ggtattttgg etegtegegg teatgaaacg atgtgegaga 600 agtaggcgag tacgggttac ctcttatcga tttggtctcg tggatctata tccattcgag 660 gccaccgtgg catcaggagc atcggagaag atatcattga gaagatagat ataggcggta 720 teteteteat tagagagetg ccaaaaactt cgaagatgte gttateatet cgteacggge 780 acagatgeeg gattttaeag cetgetgaaa gageagggag etegaacete tttgetgaac 840

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...561
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:433

gagactaaag	acactctaca	tacacttaag	cagcgacttc	ccttattggt	ttgccgttag	60
ctttgtgctg	ttaacatcca	acaagaacgg	aatggggcta	tttctttctt	tttctttccg	120
ccttgtattg	atataattat	cotocatatt	attatetett	tacttctgaa	tcagtactat	180
ggccaatcca	gracerae	tttatta	ataaattata	totgaagact	catatteega	240
ggccaatcca	ttttgttccg	ttttetttg	ataaatteta		cttaatcttc	300
cattgcatcg	agtttctgta	tgctccattg	gacgcatttt	geeeateeea	CCCAACCCCC	360
ttgggcatat	tcgctatttt	tatggcagtc	geegtaegte	agttttctat	cgggagcaaa	• • •
cggtatctac	ggtggaaatg	atctatggtt	tgttgccttg	tcatgctttg	cttttattac	420
CCAAAGCCGC	ttagccatac	tttcattccc	ctgtccatca	tggtctttt	ttggtgcgag	480
cotttttcct	tetcadaada	aaaactttgg	teacetettt	catqctaatc	atcgtaagcg	540
				-	_	561
tttatcttca	acggeettig	C				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 653 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...653
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:434

gatttggcac	tacccaattt	gcctcgaaaa	tcgagtctta	ccacatacga	tcgtaaaaat	120
ccgattggag	cattctgatt	ttctcctttc	ttccgattgg	caaaactcct	cctccgatag	180
atagatcttt	cccaacccca	tegttetget	tgccgattga	gcgtatcgtt	catgategga	. 240
tgcaagcttt	catcttctga	tacaaatccg	ccacatgccg	gtacaaaccg	aatacctcgg	300
aaatagcttc	acaagcgaaa	aactcaggac	atacaatact	gctcgcatat	aagagcataa	360
acgattgtag	actccagacc	taagggaata	tcacaggcag	cgagagatgt	aaagaggaga	420
agatgattct	aaagaccacg	agaaggcaat	gccgggcaaa	ataatggcaa	ggaagtcata	480
aagagaaaat	tttccataaa	gtatcatccg	tatttaatca	aagaataagg	atagaagtag	540
gattcccccc	ttcttttagt	gtcgtagtct	tattcaggaa	gcgcaaatag	tcatattcgt	600
ccgcttttca	atggaataac	cggcatcttt	ttccgtttcc	aagcattacc	gag	653

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 617 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{17}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

cggaagatgt	acggaccgaa	agaacaataa	accccatttt	aatctcatgg	tagtattcca	60
ttcgacctga	agtccatacg	gggattcgtc	ttcgatgtga	cggagtgatc	agccataccg	120
tttcggctat	ggatgccgaa	ggccagctat	gcgaacgatg	aatgtaaaag	acggttatgc	180
catgcaatat	gccgtcagca	aggcttcttg	ctggccatca	tcacaggcgg	atacagtccg	240
gncatgccna	aacgggcaga	atatctcggc	atcaaacatg	tctatatgcg	ttcgccaaca	300
aggtggagca	gctcgaacac	ctcctgcagg	agaccgggtt	gaagccgaag	agatagttta	360
tataggggac	gatatacccg	atctgccggt	gagcaagagg	gtggctttgc	ccqttqcccc	420
ggcggatgca	gtgccggaga	taaacaggtg	gccaaataca	tatcgcactg	ccqqqqaqqa	480
gagggcgtcg	ccgcgatgtc	atcgagcaaa	cgctgaaagc	acaaggccgc	tgggcacagg	540
gaatgggttc	ggatggtagc	ggacggaagt	cttcttgatc	gaaaaatctg	tggtttatgc	600
tggacaatct			-	-		617

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1149
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:436

				agatetatat	ataaaactaa	60
ttcgaaaggt	ctgaccctaa	tgaatgcaaa	gaacyccgll	gggcatgtgt	gegaageega	120
ctcgtgcagc	tcgtggtgca	gccgtgaaga	aacagtaaaa	aaacgtacaa	gaagcaagcc	
ggagettega	tcgaagttcc	ggctttccat	aacgaaggag	ageegeeet	gatacccctg	180
aagtgggga	acqqaqcqqc	tcttccatat	tcgagagtcc	tattttagtc	gtagcgtatg	240
aaatactgat	catcageett	ggcaatatcg	gcggagagta	caacggcact	cgcctaatgt	300
aaacuccgac	ataataata	ctctggccga	adacadtada	gtgagttcgt	ggaagctcgt	360
gggttteegg	teresetat	gcgtgtgaag	aaacaaaact	gatectgetg	aaaccaaata	420
tacggagcga	tagegegiai	gegegegaag	adgeggagee	gaecadada	atateceted	480
catatatgaa	tctgagtggc	atgccgttcg	ctactygaty	taacaggaga	acacatass	540
cgaacaggtg	ttgtccttgt	ggacgatttg	gctttgcctt	teggeactit	geggetgaac	600
ccaagggaag	cgatgcgggg	cataacgggc	tgaagaacat	tgccgaggga	tgggategat	
cgattatgcc	catctacatt	teggettggg	cgacgagttt	ccaaaggaag	gcaggtggac	660
tteatectea	accattttac	ccccgagaag	aggagaagct	gccggagctg	accaagcatg	720
coccecce	catcagagtt	tttgcctggc	caatatccaa	aggacgatga	accggtacaa	780
Cegeggagae	aasaasaats	aggatagacc	attagatata	ggctacgcgt	atctcaagac	840
ctaaggagac	ggaagaggta	aggacagacc	geeggaege	acatasacaa	actacaaacc	900
acgaacgata	gecaeggatg	cctgcaagaa	aayoogayca	acgegaacgg	ocaataacct	960
aagccttcgc	gtatggtacg	tgtgggcgac	geatteaggt	aaggaageea	transanatt	1020
attcctttcg	tattctggct	tggctcagaa	tcggatgggt	gccaagctgg	Egaaggactt	
totogaaaaa	tcactccqcc	cgaagagtat	gagatactcg	aaatgcaacg	catttegger	1080
ttatagacag	agccaaaggg	cacccqqtcq	tccgaccaaa	aaaggacggc	cgaagaagct	1140
			-			1149
tggagccag						

- (2) INFORMATION FOR SEQ ID NO:437
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 710 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...710
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437

cctgtcggag	ctactattac	gattactgta	acggtgcggc	taaagtgtgt	cagtttacgg	60
catgcaacaa	cgctccaaat	gatttgtccg	ataggggctg	attcttaaaa	cactatatca	120
gacatcttgt	gatagaacct	catggatgat	cccaacacqt	ggttcaatct	ttctagtact	180
catttgtatt	tatatatasa	tcaatacaaa	atgeetetea	catgcctact	gtaatagaga	240
aggategeet	ttageactae	agataatgac	ttcctactat	tecatectea	gctctataat	300
aatatatggt	cccgacccga	ceetecacaa	tatataataa	aaaagtatto	ccacaaaata	360
aatatatggt	acyccaatcc	gatatagaat	acceptate	assatcato	cgatagacgg	420
tgactatgcc	teceaaateg	gatatagaat	ggccaacaca	atataecaec	atcaddaaac	480
gtccttagtt	ttcactccac	cattaacctc	cetgatgeaa	acaccacgac	atcaggaaac	

acaatgacta cgtttcgccc	agccaagaaa	gaggttttgt	aaccctccat	ggtgtgaaaa	540
cgactgtaca aataatcacg	aaatggttgt	ggagtataag	attagagagt	attcaactac	600
cttcacttcc ctgattgtct	ttgcccggta	ggtcctatat	gtgtaacacg	gcaaagcgtt	. 660
atgttttggg ctgcgatcct	ccctgcgtag	aggtgcggaa	acttcggtgc		710

- (2) INFORMATION FOR SEQ ID NO:438
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...438
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438

- (2) INFORMATION FOR SEQ ID NO:439
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 826 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...8\overline{2}6$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:439

cagggtattg	accagetett	cggtgacatc	gaagggaagg	ttgatggttc	gctgatggag	60
tagtetacce	actgctggat	acatecetae	atcttcactt	ggctacccag	tccacatcgt	120
tagacataga	cttgtagtag	dacdaacdac	cacgaggtcg	tcgatctctt	cgttcgtgta	, 180
tggeegtgge	gggtcgaacc	attaataaa	atccaadtga	caaaattata	gtggtagaca	240
tttgcggtcg	gggtegaace	greggege	accoungega	gatetgtacg	ttetateact	300
acgaatcttc	gaagctgtcg	cccacttcgt	Coacacagec	t-aat	2000320032	360
cggattcacc	tttctgcgac	gcttgtagac	cggcatgaat	acegetegat	accygaggaa	420
gtctgcgtca	tcagactggt	ggaaccggta	gggctatggt	aaggcaggcg	atattgegte	
gtccgtactg	cttcatctct	tgtacagcca	tgggtcggct	tegegtatae	gggctataaa	480
gggattgttc	cttcgcgttt	ggcatcgaac	agttcgaagg	cgccgcgctc	cttggccatg	540
tanagagaget	gctataggcg	cagagtgcga	agatetteta	tacctcttgg	cgaattgggt	600
tt	gaaccgtagc	agaatcccat	cactacaaca	tatcgccttc	ggcggtgata	660
agettegtee	tacgacgacc	ggaaccccat	tacacagate	ttataccaga	ggttacgctc	720
cctacgcctg	tacgacgacc	ggeaaggeee	tacatatat	acttaggate	tattegatet	780
cgaggtcttg	acttctcgct	tegggatege	tggctatett	gettaggate	cgcccgaccc	826
tttcgcttcg	aggtcgatga	tgtcgtccat	gatgegetgt	gccaaa		020

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1224
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440

	toccaaacca	catttttcca	aacgctaaac	cgccatttta	cqaactgacg	60
tataataaa	assattasc	actcggagag	gaggtcaaca	tttcgatata	attattgctt	120
tytactgaaa	ttataaggat	carcttttc	aggagagagg	aaagagaggg	aggetaegta	180
tertegatee	tagagatgaa	cagoccccco	gagggttag	ctcccgtgag	ctgcttttcc	240
tagtagetta	cacayycyaa	gaggaggaga	ctaccattca	cataaggtgt	agcctttcag	300
aatgagateg	gateagtgge	gggttaggaa	ttcaactaat	tctcgcggtg	acaatagaga	360
caaattgtat	getetgagea	ggerraceaa	aaccatcaac	agtategeag	tagtaatgtt	420
ttgtccagat	agetaegegt	agtggccaaa	accecege	cacagacact	caccaaacaa	480
ctacagggtt	ategatatgt	agacygygac	geeggeeege	cgcagacgct	ctattttcta	540
gatgtcttca	accccatacc	catattggga	gggaageegg	tggcaagcat	cttccaccaa	600
ggatcatgaa	agccattgag	atgaateegg	ageggggeet	tegtgeteet	aaacaaataa	660
tegaetttee	acttcggcgc	catategttg	ceggagggat	tggtcgattt	tagetaeaat	720
acgaaccctc	cacatacgac	tgttgtccgg	aggeatgteg	cagatagcgt	ecgatgaage	780
cgggtgatgc	cggcaggtat	cggagtcgag	gataaggagc	tgctcgcctt	gggettette	840
tgctagcgat	tgcgcagacg	gccggctccc	atgttctctt	cggcactgac	aageggeaca	900
gtccctcctg	ttcgtaagcg	atatattgag	aagtgtaagg	ttgccggaac	agtegtetee	
aagaatgatt	tcgtagccga	cggatagttc	teggeetget	tatacagttc	ctccagcagt	960
ctgcgacaat	cccttttata	acgggtatga	gtatggacaa	ggtgggagac	atcttcgtcg	1020
tacaatttaa	taacggagta	tatgccaccg	ggctgagact	gtaccagtcc	gtccaattga	1080
ggtcgaaaag	ctgagcagaa	acatcgttta	taggtagtcc	ggtagcggtg	tcagctcgtc	1140
caccgagget	gtgcctgctc	tgagaagaca	ttcggcacgg	gggtatccgg	ccaactatcg	1200
	tcaatgtctg					1224
	·					

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...754
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

egggeaacgg etttgeaget aaaacetteg gtetgeetgt geteacgeae gggetgaagt 60 ggaagaaatg cetteteegt ceaageaact ggetgeeteg geatgttegg taegatggae 120 gaaccgccca tacaatacat tgctccggcg acgttcttca attgggagag agtatcatca 180 aggtgetttt egteeeggge actegeeegg teatetggea ttetattgee egeaggeeea 240 agctgattta ccggcgatgc gctctttgct ggcgatatgg gccggaccga cttaggggcg 300 gcagctacga actoctgaaa aagagcatto gtacggaact totoccotto cogacgatac 360 ggtagtctac cccggacacg ggcctacttc tagatagctt acgaacgaac taataaccct 420 tttctcgatt agaataatga aactaacaaa ttcgaaaacc gccatattgg tattgccgag 480 540 egegacetet egteatgete eggaceatag gegtagagte aatggateag etgateegea aacgatcccc ggcgacattc tgctgcccga gcctctcgat ttgcccgagc catgaccgag 600 egegaactge tegaacattt catggaactg ggateeagaa caagatette aceteetaca 660 teggacaage tggtatgata eggteageeg geteceatee agegeaaegt attggagaat 720 754 cctgcgtggt acaccnctat acgccttatc agcg

- (2) INFORMATION FOR SEQ ID NO:442
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...546
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

tctatcagga	tgcactcgga	cqaatqaaca	tagcactggc	ttcaatgaaa	tggtacgccg	120
			gaccatcacg			180
			cggtagcaat			240
			atgageettg			300
			gattcggcat			360
			ttggatgtaa			420
			taagcgaaga			480
	-		agacgaaagt			540
accdac		, , ,	· · ·	-		546

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...513
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

ggatatette	cgtggtacgc	tggacggtct	gacggaagaa	aaccgcctgg	attcaacagg	60
				actggcagcg		120
				gagaagaggc		180
				tgataggagc		240
				aggctgtcgg		300
				gaagggagca		360
				teggetttge		420
				cccgatcttc		480
-		atgtgctgga		-		513

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 669 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

acgaaggaac tggtgaagtt gatcctgcga aagaaaggct tcggcggctc gcttgtctgc 60 tegatgtegg caeggcaage ggatgtetgg ceateacatg geacgagaae ttegagecaa 120 agtatgggcg atggatattt cacccgagct ttagctacgg ctcgtaccaa tgtcggagaa 180 gacgaccgga tatttcttc gagggcgata ttctttctcc cgataatcgt tgggacgtac 240 tececegtg gacattateg teageaatee teegtacate atgeetgegg aaaggeegat 300 atggcgtatc atgtgctggg acatgaaccg gccttggctc tcttgcgccc gaggaggatc 360 ctctcctttt ctacaaagcc attgccaacc ttccggcagc ggtaaactac gctccggcgg 420 acggetttat gtggagetga accgetgetg geegaageea catgegaagt atttteggee 480 aaagtgggat gtgtgaagtc cgattgcaca cggacctctc cggcaagagc cgttttctcc 540 ggcaaaatat ttacccgcta acaaagcatg aagacagagg aggaactatg aatcggatgc 600 aagectactg egecegtacg gaacattgea gateagagtg geagecaaac tgegaeagge 660 agggacaga 669

(2) INFORMATION FOR SEQ ID NO:445

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 575 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...575
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

ccccgccact	gtatcggtgg	agtaatgacg	atggagactg	tctgccaaat	ccgaactccg	60
gaataatcgg	catgctcgta	tgcctcgtgc	atcaatgcag	caactgcccc	gctcccgact	120
ttgtaccctg	cttacagcca	atagagtcaa	taagaggaga	aaaagcaaga	aggggagaaa	180
aattcgtctc	atcatacaat	atatctgcta	aatgctatac	tcatctctct	cacatacgat	240
caaaaacgga	gaagtgtaca	tagcgtttgg	gattggcttt	gaggtcgcgc	aatatgcatc	300
cgcactcgaa	gccatactat	ccagtcgcat	gtagagcgat	ttgcgtttaa	gagcatcccg	360
agcgaaccgt	tggaattgcg	aatttgatcg	gaaagcttcg	aagattctct	gatgtagcct	420
gtaattcggc	catcagagcc	tcagtttcaa	ctggttcaat	tcttccgaaa	gcattgccac	480
attatccgta	tggtaccgtg	tattggccat	gacggcaggc	aattgcgtcc	cgatggactg	540
gtccaaagaa	gcnagtcaaa	cgaattaacc	cgttg			575

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...766
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

cgagcgtcgc	tateeggeet	teggeaacet	ggtgcctcgt	gatgtggccg	ccgtgctgcc	60
aaagaacgtt	gcgatgccgg	ttatggtgtg	aacaatacgg	ccttgccgta	ttcctcgact	120
				cagaagtacg		180
				cgccgatgat		240
gctatcacta	tacqatqqqt	ggtctctggg	tggattacga	gctgatgact	accacccggg	300
cctatttacc	atcggagaag	ccaacttctc	tgatcacgga	gccaccgtct	cggtgcttct	360
gctctcatgc	agggtetgge	tgacggttac	ttgttattcc	ttatacgatg	cagaactatc	420
tggccgatca	gattcaggtg	cgcgcttcag	cacggatcgt	cccgaattcg	aagctgccga	480
gaaagagttg	aagaccgcat	aacccqtatc	atgaatgtca	aaggcaataa	gtccgtggag	540
accttcacaa	agaactagge	cacatcatqt	gggacaatgt	gggaatggac	gagacaaagc	600
caatttagaa	aaagccattg	tgaagctgga	cgagctgaga	aagagttctg	gagcaatgtc	660
tatataccaa	gtgaagccaa	tgacctaacg	tagagetgga	gaaagccctt	cgattggcgg	720
		tgatggcgca				766

- (2) INFORMATION FOR SEQ ID NO:447
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 661 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...661
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:447

tataccgacc cattctgtac agtgaaaagt acaggaaaga tcaagggtta	acagcaaagt cttccaccag aacaattgga caaaggaaga tgaaaacaag	catagaagag tcaatggtta atacaatgtg agcagatatc aagaaaattc	tacgaacgct tgaggatttt gaaaatggga attacttgta caacgatttc	tgcaacaaga gagagatact gtggaaggat atcttcaaat ttgacaagta cggaggtcag	ggtcaaatag tgaagccaga ccatctgtga tctgagtcta atctgtgggt	60 120 180 240 300 360
tcaagggtta atggtggata	tgaaaacaag gagggtaatg	aagaaaattc acacaataag	caacgatttc catcgcagtg	cggaggtcag ccatttctaa caagctgcag	atctgtgggt aagtgaaaaa	360 420 480

aagctataga	aataactggc	gacagtatgc	acaagcattt	atcaatgccg	taaagaaagg	540
taccaacttg	acaaacaaat	ttcagacaaa	ccttatgttc	tcattattac	gagataaacc	600
agagggtaat	gtgtccaaaa	tattcggaga	acttatccct	tacttgaagc	tggataagcg	. 660
t						661

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1048 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1048
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448

ttgatecage teaegggtgt ggeeagtegt egagtggget taetatatgg ggetatgete 60 attgtgcttg gcttgttccc gggtatcggc ctcatctttc tctgatgccc gatccgtatt 120 aggaggaget acgetgetga tgtteggaet gageegeage eggtataege ateattgeag 180 ctcaggatat agaccgaggg ctacgatgat tttggccatc agtctgtcac tgggcttggg 240 tgtcggttga tgccggacat cttgcgcaac atatctcttg acctgagagg tatctctctt 300 cgggaattac gaccggcggt cttgctgcca taatttctaa tatcttatcc gtggcaaata 360 gaaccggcgg acaagtagaa aacccaatct tttcttatgg aattgctcaa acagaggatc 420 ttgcaagatg gcaagtgcta tccggcggta tattgaaagt cgatagcttc atcaatcacc 480 agatggattc aagctgatgt accatgtggc cgaagaattt gctcgtctct ttgccgacac 540 ggagtcaata agatcgtcac gatcgaagcc agtggcatag cccccgcctc atggtgggtt 600 acatcatgaa totgoocgtt gtottogtoa agaaaaacag cocaagacga tggataatat 660 gctgactacg acagtgcatt cctttacaaa agccgagact ataccgtttg tatcagccac 720 gactttctga cggatacgat cgtattttgt ttatcgacga cttcctcgct tatggcaatg 780 ctgccaagga atcatcgact tggccgaaca ggcaagtgct aagatcgtcg gtagggcttt 840 atcatagaga aagcetttea gaacgggaga gaggetetae agaaagaggt ataagagtgg 900 agtegetege gateateega ageettgaea atgetgeata aetattgeag aegaaaaega 960 agactaacca tacaccatto aatacacato cogtoogotg gotoagtggo gggatgttgo 1020 tttttccttc cttttctccg aatataaa 1048

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...413
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

coggacatog	aataccgact	gtccctccgg	aggagtcggc	gaagtctcgt	gcctccgtta	60
ttgagttctt	ccttcagctt	gttttgttta	teettgatgg	atcgaatccg	taacaacccg	120
acaggaatac	teccasased	aatatgacgg	tataccaata	gtcgaaaatc	tttgcttcat	180
teteteetee	ttattagata	tacatcaatc	gatgattgtg	cagggggata	tgatgctttg	240
tatgtggtga	+ -+++++++	- actataggeo	gacgattagat	cctcctattc	cctataaggt	300
ttactcttac	tetttttett	egatetgega	tteretes	acttacactt	cctgtgaggt	360
cgcgcttttg	cttctctgcg	ggttttacct	ttegggataa	gerceegger	tctgaatcgg	413
gcatactggc	tcaacgaagt	ggacttaccc	aatctttcgg	cctggctggc	aag	413

- (2) INFORMATION FOR SEQ ID NO:450
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...539
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:450

atcaatccaa	tttctttqaa	gggattatac	gatggatcca	gatctacggc	ggacgaacta	60
catttttccc	caaaccttaa	taggcaggga	tgtcgatcgt	tctttgcggt	cgaagtcaat	120
ggccggtact	gcattgctgg	agctgaggct	tcacgaatga	ccacaccgat	gagtttgaaa	180
atagectgtt	catcaggaac	ttgatttcag	ttttggtcgg	gtggatattg	acatcgatct	240
gggaggttca	agatcgaaat	acaggaagta	attgggcatc	gttccctgag	gaatatcgcc	300
tcataggcag	ccatcacqqc	tttgtggaag	taaggatgac	gcagaagcgt	ccgttcacga	360
agaagtattg	cagggcacct	cqtttqcqag	cacatcgggg	cgccctacga	agccggatat	420
attogttato	gggcttttca	tccgatgggt	atcagatctt	tctccattct	cttcccgaat	480
acatcgagga	tetttette	agaggaagaa	aggaggcaga	tectgeacea	gttaaccca	539

- (2) INFORMATION FOR SEQ ID NO:451
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 676 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...676
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:451

```
ccccggtttc cggagaaaaa ttttatcggc atcgacatca aaggagctcc atgtgggccg
                                                                        60
gtgccaaaga gtctcttcaa gaagggatgt ccaacgtact ttccttcgga cggatataga
                                                                       120
gettttggat eggttetttg eegaagggag gtageegaaa tatggateae ttteeeegat
                                                                       180
                                                                       240
ccgcagatga agaaagaggc aagcgactga ccggaacgcg gttcctctcg ctctatgaca
aagtatcgaa agggggggga cgtatccatc tgaaaacgga tagccctttc ctcttaccta
                                                                       300
tacgaaggcg ttggtcgaac tcaacggcct gcccgtacac gagtaacgga tgatctgtac
                                                                       360
ggcaaaggat gcgtagagaa tgaaatcctc ggatccgaac atattacgaa caacagtggc
                                                                       420
tggaacgagg tctgacgatc agtacatcag ctttggcttg ggagaacctg actgcgagta
                                                                       480
                                                                      540
togagaacco atattgaaat cgaacctgac agctaccgca gttacaatcg ctccagaaga
gtcaggcagt tccttcctaa taaataacct actcagaaca tggcatacta acattatatc
                                                                      600
ccaatcttat tctcgaagcc cttggtaaag ttcgctaccg gggacaggaa aagattggtt
                                                                       660
                                                                       676
tcggccggaa tggtag
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 638 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...638
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:452

ttgtgacaga	ttaccatcgg	cacaccgaga	tgtttggcat	agctattgga	cgcttcgtac	60
ctccgacatc	aggcgtagct	actacgaggt	tctctaaggc	atattcttgc	ggatgtattc	120
catgaaaacc	gtagagccgt	agagatgtcc	accggcacat	cgaagaaacc	ttgaatctga	180
tccgcatgta	ggtccacgtg	atcagacggg	taatacctgc	cttgcttagc	aggtcggcga	240
tcagctggcg	ccgatagata	cacggggctt	gtcctttctg	tcctgtctgg	cccaccgaag	300
taggggatga	cagctgtaat	gtagtgtgcg	gaagctcgtt	tggtgcattc	gatcatcagg	360
agcaggttca	ttcaggtggt	ccaagaatgg	gatgtggact	tgtacgaagg	aagacatncc	420
ggccgcgaat	gctctcctca	tggatacggc	aaattcacca	tcggcgaagt	gctcgatatt	480
cattcgcccc	gagggcaacc	cagactgttg	cagatetttt	ccgcaagata	acgggaattg	540
tcccggagaa	gacagaaaag	ttgttttcgt	tgttcatctt	tgatatgggt	agagttatcg	600
tccattgccg	gcaaatcgga	agccgtcaga	ccaccttg			638

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 688 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...688
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:453

60 cgtgtgagca acactttcct tggggccatg cagacccaga gcacttgtcc acttgccacg 120 gagagggtga gatcatcacg aagccatgct ccaagtgtag ggcgaaggtg tggagatcgg 180 cgaagaggtg atctcattcc acatcccgcc ggtgtagccg aaggaatgca aatgtccgtg 240 aacggcaagg gaaatgcgcg cccgaggagg cgtgaatggc gacttgatag tcgtgatcgc 300 cgaggaccgg atccgaatct gatccgcaat ggcaacgatc tgatatacaa tctgttatat 360 ccgttccgtt ggctataaaa ggaggtagtg tggaagtgcc gacatagacg gacgagccaa 420 gateegeate gaggegggga cacaaceegg cagatgetge gtttgegeaa taaggggttg cccagcgtaa acggctatgg ctgggagacc aactggtgaa tgtcaatgtc tatatccccg 480 540 aatcgatcga gccaaagatg agcaggctat cgcagcgatg gaaaactcgg acagcttcaa 600 cctaccgatg ctgctcgtaa ggatatagac aagaaataca gagagatgtg gattgaaaga caatgccatt gtatggtact tgacctgaga aaagctgcgg tatccggtat gcagtttgac 660 688 aaacgaagtc tttttgagcg atgaacac

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1311
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454

```
ggaaagttgt attegggtea tgettgettg etgegeetgt eegtttetee aggetatgta
                                                                        60
ccgccagcgt gaaaagttgg agaatatcac agttttccca tgttgtattt cggcgacggc
                                                                       120
geogeaectt geteegaaa tgegtteeat gtacaccega eteteaactt eettgaggge
                                                                     ~ 180
aactcccgtc cggcaaccgt gaccgtcgtg tcgatttcat tccctgccac ttccacgagg
                                                                       240
taccgaactg tttcgtcagg gattctttcc attggatgta gccgtagtgc aggttctact
                                                                       300
cctaacgaag agggttattg ctctttcgga gtttcctgcg actcacaaag gctgccgccg
                                                                       360
agtgcgctcc ggtagtagta gccgaggtga acagcaaatg ccattcatcg gtggtgaaaa
                                                                       420
cctgattcac atctccaaac tacccatatc atcgaagtgg acgagccgat tgcagaagta
                                                                       480
ttgcctcctg tatcagcgac cttgaactga ggataggtca gaattgtgcc tcactgatca
                                                                       540
agacggcgat accetecagt tgggtategg eggtateece gaegetgttt gegtgeattg
                                                                       600
gaagggcata aagatctcgg tattcacacg gaaatgttac cgacggggtg atgcgtatga
                                                                       660
ttcgcaaggg gattatcaac gggaagaaaa aacattgcat cccgaaaaag tcgttacctc
                                                                       720
gctaatcttc ggatcaaaga attgtacgat tttgtcaata acaatccggt gatagaatgc
                                                                       780
tatoggtgga ttatatoaac aaccoogatg ttatoggtaa gaatgacogo atgtttotat
                                                                       840
caatteetge ttggagatgg ateteatggg geaggeaget tegagtegat egggtaegaa
                                                                       900
cagttcagtg gatccggagg tcaagtcgat tccttcgtgg ggccaagcgt tccaagggag
                                                                       960
gaatctccat tatggctttc ccagtacggc caagaaaggg actgagagtc gcatcgttcc
                                                                      1020
cattetgaag agggtgettg tgtcacgace ggeegtaacg aagtggacta tgtggtgagg
                                                                      1080
aatatggcgt agcgcgtctg cgtggcgcaa cgcttcgtca gccgtgcgaa gccttgactg
                                                                      1140
ctatagcaca tecegattte gaceggeeet tgaggagaaa teegeegaeg ettegaataa
                                                                      1200
gtcggaagga ttttaggcct tatataacgg attcgaagcc atgttcaact acattgtgta
                                                                      1260
catggetteg tatgttaacg tgagtteaat gtaagegata tggtqeeqat t
                                                                      1311
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 562 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...562
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:455

```
cggcaaaggg caggctgcga gcaagccgct cgagggcatc gttgttcagc cgaatccgaa
                                                                        60
atgacgaget aacaggatat aggeegttge attecaatea tggaegtaga cagatagage
                                                                       120
cgatccactt cggcagcctt acgctccatc gttctacgac gagcgtgtcc agccagtcgt
                                                                       180
ggacttcgag gctatcagtt catggageet gteettacaa eeeggeaaaa gggaegteeg
                                                                       240
gagcaaaagt cggcgtttgc cctaagccgt tcgtctacat gcataacgca aacgggacag
                                                                       300
gttcaccgct gattcggtgc cgtatcggga ggtcatccgt ctcaccacat ggagtactac
                                                                       360
attgtcataa gccggatcga gatgatgccc gtacggaccc aatccgaagc cctgcaatga
                                                                       420
atototacgt tgccggccca gggagatcgc ccactttcac cttggcgttg aagaaatcgg
                                                                       480
ggccactatc cgattgagca ttcccggatc aatgacctna ggctccaaaa agaaagcatc
                                                                       540
ggcccatagc ttaacgagct at
                                                                       562
```

(2) INFORMATION FOR SEQ ID NO:456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...536
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456

gateceegte eggteggtge	cagcagttca	caatctgctc	cctgctcgaa	atagtctgca	60
ccacagaage gataagetgt					120
ataaggttcc ctgtcgaaca					180
gtcggggtaa acggcaattt					240
aaatctatat ttgcggggac					300
caatacggat taggaagcgt					360
tgaagacttt aatcaagatt					420
gatgagcata tatacccccg					480
atccaaaaga gctgaaaaat					536

- (2) INFORMATION FOR SEQ ID NO:457
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...550
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457

teceeggetg	ccgactcata	tcggcaaagt	cctgtcccgg	ctctttggaa	ttctttccaa	60
				ctgcaggggg		120
				cggtatcagc		180
cctcttgctt	ccacagtcat	cgttccgctt	gtggaagtag	tcgtccgaca	gacgctgcca	240
agcttctttt	cctccaagct	cagatgagca	tagcgaaaag	acttttcgaa	atggtgcgtg	300
-				tactctgtgg		360
caaacctctg	atcgtgtcct	ctcctccgac	aaggctgtag	gatctaacgc	tgctatatcg	420
				atcgaacgga		480

gacagcatac tegettgeat agegteegaa aatetgettg aggteatetg catgaacgag 540 eggaagggag 550

(2) INFORMATION FOR SEQ ID NO:458

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1099 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...1099
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:458

tectgggate aageaaatte aggtaggtga geetageeee taccageeet ttecaacttg 60 acagctacaa cgcagggtca gaaagtaacg ctcaagtgga agcaccgagc gcaaagaagg 120 cagaaggttc ccgtgaagta aaacggacgg agacggtett ttcgttacga tcgaacctgc 180 aaacgatgta cgtgccacga agccaaggtt gtgcttgcgg cagacaacgt atggggagac 240 aatacggtta ccagttettg ttggatgeeg atcacaatac atteggaagt gteateegge 300 aaccggtcct ctctttaccg gaacagette ttecaatett tacgtgegaa ettegagtat 360 420 gtgaagttgt aatccccggt gtgtttacga ctattgcatt acgaacccgg aacctgcatc 480 cggaaagatg ggatcgcagg agatggaggc aaccagcctg cacgttatga cgatttcact 540 tegaageagg caagaagtae acettteaeg atgegtegeg eeggaatgga gatggaaetg 600 atatggaagt cgaagacgat tcacctgcaa gctatactat acagtctatc gtgacggcac 660 gaagatcaag gaaggtetga eegaaagaee taeegegatg eaggaatgag tgeacaatet 720 catgagtatt gcgtgaagtt aagtacacag ccggcgtatc tccgaaggtt tgtgtggatt 780 atateetgae ggagtggeag aegtaaegge teagaageet tacaegetga eagtgtagga 840 aagacgatca cggtaacttg ccaaggcgaa gctatgatct acacatgaac ggtcgtcgtc 900 tggcagccgg tcgcaacacg gttgtttaca cgctcagggc ggctactatg cagttatggt 960 tgtcgttgac ggcaagtctt cgtagagaaa ctcgctatca agtaaatctg tcttggactc 1020 ggagactttt gcagacactt ttaagatagg tctgtaattg tctcagagta tgaatcggcg 1080 cccgacctcc ttttaagga 1099

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1133 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1133
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:459

gctaactatc	aactgtttgc	aactatttta	taggactttc	attgaagtct	ttgccgcaga	60
gctgattctt	aagtgttttt	cagattactt	gaggtttgag	agagatcgca	tgaagctctc	120
ctttcttcgt	caaatcaatg	cttgtgttgt	cttgatcaat	atgagagggg	gttattgtgc	180
			gtatagaaac			240
			gacagcaata			300
			gatttcgctt			360
			tggtccaatc			420
			tttggggtta			480
acccagcate	tgcgagcaaa	cttcgtcttc	acatagcgca	gacaagcctc	tgcctcgttc	540
			tatcagtata			600
			ccccgagcat			660
			gatgtaacta			720
			gccatcttct			780
			agatattggc			840
			ctcttggtag			900
			gtagaggatt			960
			catcccaatc			1020
			acatctacag			1080
			gtcccaaagc			1133
J J	-	,				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...421
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:460

atcadctctd	саасаааааа	cttcaatgaa	agtcctataa	aatagttgca	acagetgata	60
			gacaatcggt			120
						180
-	-		tgcaggaagc		_	240
-			tgacaatcgc			300
			gtgcagggag			
gtcctgcatc	atgcagggag	caagaaacag	ccgacaatcg	cgtctgcatc	gtgcagggag	360
caagaatcaa	ctgacaatcg	cgtcctgcat	cggcaggaag	caagaatcag	ccgacaatcg	420
t						421

- (2) INFORMATION FOR SEQ ID NO:461
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 635 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...635
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

ctagaggate eeeggeaggg gatteeegtg aatataggte eaetgggeat ggeatteagg 60 cctatattcg actccaaagc ggaagtgatc caccacgcat ccccatggat tcggcaatcc 120 ttatccattg ctccgtgccg taaaaactcc gacaagtgaa ggcttgagta cgatacaggc 180 cggacggata taagccacat ctcccgtttg gaagtttcat cgtataagcc tatcaattcc 240 tcatcaaggc cacggcaaca ggggcattcg ccgcaatcct gcgcatagcc gcgtattccc 300 gtccctgacg ggttgctcca ccgaatggat accgaaggcg gataacgttc caatttatac 360 ategeeteet ettettegaa ageeeegtte getegagaeg aataaeggea teetteeega 420 atttctcgcg gaccatccgt acaaagcgag ttccgattcg aaatcgatag ccccgatttt 480 aagttttata ageggaaage ceteeteeag ttteteetee acaegeette geatagettg 540 aagetteeca teeatateaa aeegttatgg gaateeeege ttgeeggagt gaaageegag 600 ggaaaaagca attccccggc ccttgaagtc ggcaa 635

- (2) INFORMATION FOR SEQ ID NO:462
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...307
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:462

60

120

tgtaaatcat actctttgt gattctcggc tgcataatga tcgggaagaa ggggcggctt 240 ccaagtcatt gggcttagat gtagataaaa agccatctga aagcaatata agtgtctgaa 240 aaacatgtgt ggaaaataaa acacataat aaccaatgtg ttgtgccatt ccttatatcg 300 aactcac

- (2) INFORMATION FOR SEQ ID NO:463
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...509
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

aataaaacac actaataacc aatgtgttgt gccattcctt tatatcgagt cacgttaaga 60 aaagaccaat ggtcatatcg caaaaatgcc gtacaatgtc tctaataagc cccctgggcg 120 atgttgtact tettetegat ggcatactge teeggggetg eegaggtatt ettecaeaat 180 gtgaagacgc teggaacggt caaatgttte gacatgatta etgettttt tgacetetee 240 gattcgtaca cgtcagttcg taaaaatgga gacctttgca aaataaggag gtgggggaag 300 aggagttett ggcaaaaaag gagegagtga aaggggtgge agtaggagtg aaagtagttg 360 taaatccccc cttgaggagc tgcttgcacg agtcctcaag gggggttatg ccttatccta 420 gagatgagga cataattatc cggggtcctg tataaattaa aggcgatgct ttcaagaatg 480 509 ttttgagtat ggtcttggca agtccccgg

- (2) INFORMATION FOR SEQ ID NO:464
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...519
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:464

tctcaagggc	gagaacattc	gccccctcgt	aacgaaactc	ggcgtgacgc	actcgttgac	60
agactggaaa	agaacaataa	ggccttcgcc	gacttcttct	ccgccgtctg	agcaccgacc	a 120
aacgaggcaa	atatgacgtg	aaggcacccg	tgccgagacc	gaccgcacat	tggtagccgt	180
ggtgcgccgc	atggacccat	cgacgacatg	gagccgagcc	cggagatccg	tgcgctcatc	240
gagcttacaa	ccgactcgtg	gccaatcgcc	gegeeetett	ggctcgtcgc	gccactacgg	300
agaagcagcc	gtggagaagc	gtcgtgccga	gatcgccgag	atgtccgccc	cctgctcgcc	360
cggatcgtgg	aggagaagaa	gacggccgtc	ttgccggtcg	caccctcggc	acgggcaaga	420
accgccacta	tctcatcaca	tcgtagccga	gaacggcgac	gaggaggatc	gctggtaccg	480
catcgacggg	aacaactcgt	ctatgtgccc	gaagacgaa			519

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 912 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...912
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:465

```
ggcccaaggt cgggagtttc gacggaggtt tcggttcttc ttatcttgcc gttgtgtagg
                                                                        60
tcagaagaag acgagggaga tctggttttt atgccgtcgt ataccgctgc ggaggccgaa
                                                                       120
gctatgggga tggtaaacaa ggtggtactg ccgcgaggtt ggaggacgaa acggtggact
                                                                       180
ggtgcaagac gatattagcc ggagtccgat ggcgatccgg atgattaaac gggctttgaa
                                                                       240
tgcgggctcg acggtcagag aggattgatg gagtttgcag gggatgccac cctttgtatt
                                                                       300
atcttatgga agaagctcag gaggggaaaa atgccttttt ggaaagcgga ctccggattt
                                                                       360
cgacaagttc cctaaattcc cgggttgatg ctaaggccga ttatatcccc tataccttga
                                                                       420
aattcaagga geeggeaggg agtegegggg egttttgeat accaageaga ettatttegt
                                                                       480
gagggtatac acgatacttt cccctctcgg gcaggttacg gcgaggcggc tttattccgg
                                                                       540
gattgagtgc ggaagaggga gcggattacg aagagcggct ggcggaggtt gcaacggcgt
                                                                       600
ttgcgggttt actcccgacg cctggcaggc atatcctctt tgtgtttcgg gatggaaacg
                                                                       660
gegettgeeg acttegaggg egggggttge ttttteeete ggettteact teeggegagg
                                                                       720
cggggattcc cataacggtt tgatatggat ggggagcttc gaagctatgc gaaggcgtgt
                                                                       780
ggagagaaac tggaggaggc ttccgtgtat aaaacttaaa atcgggctat cgatcgaatc
                                                                       840
ggaactcgct tggtaccgat ggtccgcgag aaattcggaa ggtgccgtat cgtctcgatg
                                                                       900
cgaaccggct tt
                                                                       912
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 734 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...734
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:466

ccadaataaa	cacgaattaa	tgtgttagag	atcctaattg	tagaaggaaa	gaccaaggcg	60
gagtagaacc	tttcaaatgc	gatageeece	tgccgaaggg	ccggcctctt	cggggaattt	120
tatataatat	ctattactct	tactattgaa	attacaatca	cgggtatctt	tctattataa	180
zzestaataa	ttcasascca	caaddaaatc	gaggtcatca	atctgctatt	gagtctccga	240
ggaatggtgc	220000000	aaccttatct	ttatttaact	tagcattata	aagttgaagc	300
gettecaaac	aaggggggaa	ant+++++	tatttctttc	cttttatggt	cagtaccatc	360
agttttctt	tegtetgtet	ttasttagga	addcadtcdc	ttcttgttac	tectacagge	420
tgteggeeag	accegagett	cegactegeg	tataaataat	ggggaaggac	teeggattag	480
acaaacagtt	gaggetatat	cetaetaeca	ctacaacage	gaggaagga	ctgtggtcag	540
ttttgatctt	tgggcgatga	gagtatgacg	ecgggacaca	gaccycagoa	ctgtggtcag	600
attggcaggc	gagtccggtt	teteeggetg	aagetgttte	atasttacas	agaacgaatt	660
cgatccgcct	gccgttagca	gagetaettt	ggicaacacy	gccactatga	actggctttg	720
cccaatgcga	attgcacccc	aagctccggg	aatatctcat	gadeguateg	acgttatgat	734
ccggacgaaa	cgct					,54

- (2) INFORMATION FOR SEQ ID NO:467
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 943 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...9\overline{43}$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

cagattcagt	ctgatcgcct	Ctccatatas	2000000tas			
- 55	·	cccgatatga	ageegaetea	Ctaagaaaat	cgaataccag	660
ggtatcggat	tcgccaatcg	attggatata	tegeteeett	attcagcatg	agtactgctc	720
tttcggagcg	gtggtgcttg	ggataagttt	cggcttaggt	tatttqqqct	tcaaacaaac	, 780
gctgccgaca	tatccgaccc	gaagagggaa	ggttacttct	CCGGCaGCaC	agtggagcca	840
atacggcact	caacutauga	tacaacetes				
	caacgcagga	cacaagetga	acaaacattt	agcatcgggg	gagagatcat	900
gatggtcggt	ggcgttttcc	atccggataa	ctaaagatga	cga		943

- (2) INFORMATION FOR SEQ ID NO:468
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...524
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:468

gccagaagta	cgtgagcgag	ccggtctggc	aggtatatct	ctctgagtgc	cttcccatgc	60
agcagcgtcg	aagcctgaat	ccaaggctta	tgctggtgtg	aatccctccc	tatqqaqaac	120
gtatcaaagt	gaggacatgc	agcagtttat	accatgatcg	gagagcgact	caagcataat	180
tatgcaggtt	gctctgatgg	attctggctt	tcaagccgga	gcatttcaat	catatoggco	240
ttegtagtet	catcgagaaa	agttgatgaa	tggagctttg	gaatgtgagt	tgcgggttat	300
gaactctttg	agggacgacg	cgattcattt	gccgaaagaa	aaatcgtcga	gccqaaqqaq	360
aacaaggegt	aggacggaga	atcgaccgtc	gtacgtttct	gccggaaggg	aaaaacgctc	420
caactccatg	gatcgagaaa	aaagtctcct	tatcgttctc	ctcgtcctga	taagcctttc	480
agaacttccg	taaaaggaaa	aaagagcata	atgatgagca	gcaa	•	524

- (2) INFORMATION FOR SEQ ID NO:469
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION $1...4\overline{98}$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469

gggcggcgag ccggtttgga tgggtaggat ccgaaacggc ccaccgttcc gtttcgtgac ggagcgaccg cgcttgtcat acgccgaaag cccgctgaca ccgcaagcgg ttggactctc cacggtatgg ccacgtacga acagtttcct ctacatggcc	tgtgaacgga cgtgccgctc gtggtacatc ctggcaatgg tgcccatagc aaatgagaaa	aatcggcctg cgtcatcgcg gaggagccgg tagagcggtt cgcacagacc tggtcaatct	gcggtggaaa tggctcggac atatgatcgg ggacagtgtg gactcatcat gtcgcattat	tgcccgaaaa acacagccaa gtcgctattt agtatccgat ctgcctgcgg	60 120 180 240 300 360 420 480
acagtttcct ctacatggcc cgagcgagcc atgagatc	aeggggeett	Cacceacteg	caccegaage	000000	498

(2) INFORMATION FOR SEQ ID NO:470

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 882 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...882
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 511 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...5\overline{11}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:471

ggggttctgt ataaattaaa ggcgatgett tcaagaatgt tttgagtatg gtettggeaa gteeceggta tegacategt eegecatgaa accaeeggga ataetgeeaa aggtgeegtt eegatggtge teegtategg aeegattett tgttteettg ettetettee teggteaatg eettgtgeggtt tgtgeettgt geatgatgee gtettgaagg tgatgggtt geaggtagaa aegatteee egeaageata teetttgtee geeaagaegg ttgeeettga gggttgtttg eaeettgeaa tagegeaata aeetetteg tgteaetgeg gttgetgeaa gtegttatea eettttgaae aatgeettga aeattggtea gaaatgettt ttgtateegt agtgataaeg	120 180 240 300 360 420
certificate daigeettga acattggtea gaaatgettt ttgtateegt agtgataacg	360 420
cttttgtttg taaacccaac ggcttcttca tecgteeett taegettgac ggacaacctg tttttgataa cetectetge etettttee t	480 511

- (2) INFORMATION FOR SEQ ID NO:472
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1211 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...1\overline{2}11$
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:472

atctatcaca ttcgta	acca agaacagcaa	cgaggaggat	cgctggtacc	gcacaacggg	840
gagcaactcg tctate	rtace egaagaegaa	ctccccaagc	cgagaaaaag	aagaaacccg	900
caagcagcac ggacac	toca tocgagoogo	cqtcctgccg	gatccatcgc	aaggaggcag	, 960
cagtagegge ggtgge	gage aggetetace	ggcggcggac	tetgatecee	ccgtgccgtc	1020
ctgccggccc agcago	acag gcaaccgagt	ataaaagaca	aaggggctgt	gaccaaatca	1080
tttttggcac agcccc	ttgt atattcgaaa	aattaggtgt	tagccctatt	agccttttc	1140
tctgnttaca aactat	gtot aaagaaaagt	ctatgcagga	cttanccaac	aaccgcattt	1200
tcttacttgc g	, ,				1211

- (2) INFORMATION FOR SEQ ID NO:473
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...512
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:473

ccgtgcgcgt	agagetaaaa	tectetatag	ggataaaggt	cgaatcagaa	ctgtattttg	60
ctcaagcaat	tggctataaa	tagcattctg	cgcttattga	ttttgtttta	ttatctgcat	120
tcccagaggg	aagagtcggc	tgcagggaat	aaggatcgca	gtggaatcgg	tttctgcctg	180
tegeacateg	ctcaqcaatc	cacaggcttg	agttgccagc	tecetatetg	ctcgggcaga	240
tagaaaaagc	acccaaaaga	attgccgttg	cagcaagcaa	caaccaaaaa	cgagcatttg	300
attacgcggg	ccttccatag	aataatcttg	tgtcggattt	ctctctttgt	agaagaatca	360
aaaattgtgc	gcaaagataa	acgttacaca	agaacttgta	ttaaccatcc	tgaaacgaca	420
ggacaatcgc	atttgaaata	tagcctgatg	atgctccgtc	cggaataaac	acgaattaat	480 512
		gaaggaagag				512

- (2) INFORMATION FOR SEQ ID NO:474
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1949 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474

cggcatactg aatgcctcgg gtcgctatga tgaatcatat ggctcgtata tttgatgctg 60 atcgtagaaa caaaggcttg atgtagagca ttcaaacacn ttcaacttca gggtcggatg 120 taagcaatac cctacgatac agcgacttag gcatcggtca gtagggagag ataggcaaac 180 ccatcttggt aagccagtag gtgatgtctg ctacaaggag ttccccaggt ctttgaggca 240 caaactagge tetgtattga geaggtette atacttgtag ageetatgee gagattggtt 300 gtccgagggc gcacagaccg tttgcgcagc atcataccat ggctctgagt agggcgcaaa 360 agegategeg cecaagegtg aacttgggge egagtattge tgacaaagea ceatgagete 420 teggaageeg gettgaggta gtgetetget tgtettaagt gecaacaata ttggatgata 480 ctactgcata gacatcctcc tcatgttgtg ctaaatcgtt gagatgacgt ttataaaagc 540 ctgacggcta aagccaagca gttcgcagag tcgagcaata ggatacctgg ctccggctct 600 gataaacggt gaactacttg gcttcggagt tttttcgatc tgaatgccgt aggtttcttc 660 tgccaactet acaagtaget tgtaggttga tgccctagtt ettetegett gagacgaete 720 ttgaggacac gatttettta egtagetget ctaactette ttttteatte aggggtaget 780 cacttggggg gattgggaca ctttcattgg gaccggatga actttatctt cgatccaaat 840 ttactaagec aagagegaat gagaceatga ettagaceat attetgetea atggetaett 900 tgctatctga ccccgagagg taatcctcaa gatgctaagg cgttcaaagt tgtttaaatg 960 tttgcccata atggatactg ttgcatcccg cccaactgtc aactttttc agtacacgtc 1020 aactttettt gatttgtggt tegaetttte etgatggate gaacgettet tettegtagg 1080 tccggggcca tgcagagaaa atggtacata actaacggag ctttagcact ataaaagtgc 1140 ttagaaaget gtttttgatg egteaaceet geaacageet etgteateta tttggageaa 1200 atteatacce tttegatete agtegaaaag caaaacggga aaaaccgaaa aaaagaatca 1260 cttcgatcga tcgcttttca tgctctgaca agtaaaaaca acttgcatgg agaaagtatc 1320 ctttgcgaca ttttgtttgc cgcagagcag gcaaacagga ataagtctcg ggtgccatcc 1380 ttttgatgtt gaaatgcgat ttgcgaagaa gccttcgccg cttctttctc tcgcggacag 1440 gcatggaatc caaatatttt ggagcggaat tettgtgaat gaaaaaaata teggaacttt 1500 geggeegttg egattggtet tateacetga aaattatttg atagggeteg tegeattetg 1560 gtaaaatcac cttatcaaac tcagtatgct atgacggaaa aaactaccgt aaaaacgtga 1620 aagatgttgt agtccgattc tgcggcgact ccggagatgg gatgcactga ccggaacgat 1680 atteteegae ettteggegg tgtttggeaa caccatteea ettteeegga etateeggea 1740 gaaattegtg etecacaagg gacatgggeg gagtateegg attteaagtg cacateggaa 1800 enegatetgg tactactece ggcgatttgg etgacgttet egtageeatg aaccetgeeg 1860 tccaaagtta accggacaca cgtaagacgg gactncatta ttattantcg atctgactct 1920 ttatggcatc tgatttggag aaagcagaa 1949

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 691 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{9}1$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:475

		acataaaaa	ADDDARADDA	gctttagcgg	cagaggcagg	60
gctgcgatag	egicagiteg	acgigagaaa		assecurata	tcaccataaa	, 120
attgctattt	caatatatcg	gataageegg	egaacaaceg	aaaccggata	-tteastage	180
aataacggct	acgatgcggt	tgaaccacgt	atgccaacga	cattgatacg	accycycage	
aggetgaaaa	gataaggata	agagaccacc	agccaatcgc	ccccaaagct	atacctaaca	240
tuesassassassassassassassassassassassassas	taaccdacta	acatectece	cagaacatna	gtgacgaagt	tgaacgggaa	300
tgeegaggta	taaccgacca		gagttagata	dedaaddeda	aaagagetta	360
tatagagcga	taaaaaagaa	aatyataaaa	gggccggaca	gcgaaggcca	tagatagaat	420
ggacggtatg	ccatacagag	tagttattat	cctatcatcc	accttgaagg	cyggegeage	480
ccdatacada	tatataccga	angaaacatg	acgacactgc	cgaagaagct	gtagecaage	
ctcattactt	traatgaagt	tcatcaccaa	acctattccc	agatacgtga	ccagtggcaa	540
cccgccgccc	ataaatataa	ctcccattac	ccaatataaa	atccaatccg	ccgtcccctg	600
gaagagateg	Claagtatyg	ccccgactac	estagges.	taggaggggg	acacgagaat	660
tgcagagtcc	ttcgaatacc	acaaaattcc	gategggeea	caggageeeg	acacgagaat	691
gcccatgaga	atacccgtat	agaaataagt	g			051

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 638 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...638
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

teggategat attggaagtg geeggttgga etgecaatac agtactteeg cattegagat	cgaagctgtg aaccctgatc ttatcaggtt gaaaaactga atctgcccat gttggcgctt	aagactgttt tggaagacaa aaggctgcaa tagctcaata tatggagaaa tcggnttaat taaggtaatt	ecgacetgtg ccegaacteg atgetgeega aatgeageet gcegeeaaaa egeteegget ategetgetg	gaagtagaga ccggtatggc	tccctacggt ctcctgagtg tcatatgggt atgcagattc cttttgcaca agcttcattt	60 120 180 240 300 360 420 480
cgaggccaga gtgtggcgta ttgacggaat	gctcgcggta ttgcttccat ggatgctctg	taaggtaatt gacgtctatt	ategetgetg eeggtaatag tteaaatgee	gtgtacccat	agcttcattt caatgccacc ccgttgctac	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...491
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

ggacatgaac	aaaatagccc	aaatgagctg	caatccggct	gtcggaggat	agctaagggc	60
cagatagtca	gggagataga	cgccttaggg	ggacgaatgg	tatcgtcacg	gatgctacgg	120
ccatccagtt	tegtatgete	aatcggacaa	aggccctgcc	atgtggagtc	cgcgcgctca	180
gagegaeege	atgcgctcat	ggaagcgtgg	cgcgatatag	tggagcacga	gcctaatctg	240
tacattggca	ggacagtgta	cgctgcctct	ctattcgtca	gggtgccgtc	gcggagtcgt	300
gacggctctc	ggggtagagt	ttcaggctcg	taccgtggtg	ctgctacagg	cactttcctc	360
ggaggtgtca	tgcacttcgg	ggagcgtatg	atgaaggagg	acgaatagcc	gaaccggctt	420
cccacggcat	tcaacggagc	agcttcgtga	tctgggcttt	cagaacccga	cagaatgaag	480
accggggact	С					491

- (2) INFORMATION FOR SEQ ID NO:478
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 586 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...586
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:478

gggagagcgc	atagcccgat	ttgcagatat	agaagtactc	agctatcqac	cgacctcttc	60
ggcacattga	cccctaagca	gaggatgctt	tgctaccact	atcggaagca	gccctgcgag	120
gacgggatat	tacaaccata	cagaactccg	ctacaacctc	tgggtacgca	gtctgatgga	180
gegtatttae	acccatttag	caagtcggaa	cgaaccgacg	acttttqccc	toctogaaga	240
ataccettet	gcatctggtt	tgccaatggc	attcaccacc	attacagogg	agccaattca	300
rigecegttt	cagtccgggt	ttcttgcggg	cagccctgag	agagcqqqcq	tagaactaga	360
gccggaagag	caggtgcttt	tggagcgcgt	atgtacgata	cccgattttc	tacccaaaca	420
gaccgagcag	agcggcgaag	agatattatc	aaggcttctt	cggtcaattt	ctatgcaccg	480
ggtateaccc	agecegaage	ggaaagccat	tacaaaaacc	tgatagaaag	cttctttccg	540
aaaacyayaa	aaagcttgtc	cgccgagctt	tcggactgga	aatacc		586

- (2) INFORMATION FOR SEQ ID NO:479
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 636 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...636
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:479

gogatatact	tgatggcata	gtcaagcgaa	acqqaaaqgg	gttcggtatt	tttggcaacc	60
gegacacact	acctacatac	ttgatataag	ggcgaaggt	cctacggcta	ccattacatc	120
ccacaaaccc	tattataca	atttattaac	aggaggaata	gttccaaagc	ttcctccagc	180
egeateetea	cattgeetea	cccactage	acaaaacaaa	ctgcgccttg	ataccgtttt	240
gtgatggatt	egatggetgt	gaagataga	tocatagoat	cccatttttg	ctacacagat	300
ccttaccgtg	cgacetttet	geaceacege	ctttcaccaa	tctctaatca	ggatcgaact	360
teteeggtea	caggateegt	accoagcatt	tatatagaac	tetetggteg	gettetgeea	420
cgcatgcttc	tgccaccaac	gggtggaatt	tettttaa	cgaccgatct	gaagttgtaa	480
ttgcagtttt	ccttcggcta	ttggtcaaat	tttana	ctttggccgt	atatcagtgg	540
tcgatcacct	agggaacgaa	gccacgagaa	agtegtteac	cacaagcccc	ataacttttc	600
gaggagctta	ttcnggtcct	gtccgttcag	tteegtttga	tegteteett	atggcttttc	636
cccttgtggt	attccagcag	gatgtattcg	cgtgtt			000

- (2) INFORMATION FOR SEQ ID NO:480
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...350
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:480

tactctccgg ctt tgagttggac agg ccggaccaac tgg tgttgtggcg gna	accacca aagagcaaaa tttttcc ggtgctgaga aatagag gcgatctaca tgatact ctccttgtgg ttgctgg ccgacctttg	ttgctttctt ggcagagcgt gtaataatat ggcgcaatgga	taaacttgct cgttttggta ttgataacga	gtatcgacat gtctatggtc tgcttgatcg	60 120 180 240 300 350
togttotoca ato	ggcctta tccactatca	tcatactgtt	tacggggaat		350

- (2) INFORMATION FOR SEQ ID NO:481
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 823 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...823
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:481

tetgeggate ageaacggta etteegegae eteggeaaag agtatgeege ateaaceete 60 ctttctccga acagtgaaag acnacggcag gcttacagat cggactctct tttgaatatc 120 cccatcttct ctgccatgca aacgcaaatc gcgttcggag cagtcgcctg caaatacgct 180 caagcgagct tcgactgtcg aagagaaaaa agccctctat aaagagatca ggcaagcata 240 cagcatgeeg tggeageega taaggeeate geageageeg aaaacageaa ggeeetaege 300 tcaaggcata cgaatacgct cgcgacagct tcgaggcagg gcgttgtctg cctacgaata 360 tgccgaggca aaaacaaaat acgccctcag ccagtggaag aacttcgtgc caagtatgac 420 ttcatataca aagccaaagt ttggatttct atcagggcaa agacttctaa aagactcaca 480 agaaagctat tttgaaccct cagcgaggtg ttcatgagat ctatcaggac cccgacatct 540 agggtgctgc gtcaaaattc gttttgccac agcacccttt taacgtcatt cgacgtaaga 600 aaacgccaat gaataattot tttootgato agagattatg coctaagatt ctooggcaaa 660 tgtatagggg gtatcctgct tctgctggat cgaaccaaca ttgaaattcg gattgctttt 720 gacagaatgt tgcagccgca caggaagatg ggctatacca cagggcaaga tgccggtact 780 ccgtgaggat gatgggctac ccccgtatgg ctcttcgagg tac 823

- (2) INFORMATION FOR SEQ ID NO:482
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 563 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...563
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:482

ccatggcact	ctgatgatcg	ataattccag	tgctttccgt	atgcaggaaa	cgttcccctc	60
gtagtaccaa	aggtaaatgg	ggatgatgcc	ttggtacacc	tcgcaatatc	atctccaatc	· 120
cqaactqtac	aacqattcag	atggtggggc	actcaagccg	atagaagacc	tttctcacat	180
			gccagtggtg			240
			ggggagagaa			300
			gatcgacgtc			360
			aacgtatcat			420
			tgcccacttc			480
			gcagcctttg			540
	tgagcccgtt					563

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...442
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:483

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484

gccccacgat gagaagaata gaattgtaag caatcctcca cgatctcggg tctgatctgc 60 tttttcacca cgatgagaag aatagaattg taagcaaaaa tgagtccgaa ggaacgcatt 120 atcatgggag tagacccgg cacaatatga tgggctacgg gatgcttcac gtcgtgggga 180 atacteceeg acteatgeta tgggggtaat acgtetggag aaattegaca ateactatat 240 ccgtcgaaac gcatattcga caggattaca ggtctgatcg atgaattcct accgatgaaa 300 tggctatcga agcacctttc tttgggaaga atgtacagag tatctcaagt tagggcgggc 360 teagggtgte getatggeag eggetttgge teegacatte etattaegga atatgeteeg 420 atgcgcatca agcaagcgat tcaggtaatg gcaatgcgag caaagagcag gtagccggca 480 tgctccaacg tatttacgaa tacctgacga acagatgtta cctgaaatgg atgccacggc 540 ggactggcgg ctgccgtctg ccacttcttt cagacgtcgg gacctatgct cgttcgggcg 600 gateggeagt caagaattgg aaagaetteg teaacegaat eeggataagg taegetgaeg 660 tttgtgtcgg cctctttgtt ttccttaaaa acggaaccgg agaatcagag caaatcactg 720 gccaattege teageegett egttegeeet tgateagatt gacatgggeg aagageggtt 780 gecetteate etttegatea tataggecaa teegttgete tgggeatega ggttggagag 840 tegatetgtt egatgtegee tgtaaaaate agettgetae eteteetgea egggtgataa 900 togttttgat ttogtgagga gtcaggtttt ggcttcatcg acgataaata togtttccga 960 cacgctacgt cctctgatgt tgccaaagct tcgataacga gcttttcggt tttctgcatt 1020 tegiceaget geggagiteg eigetatitt gageeaactg teetitgate acatteagit 1080 gtcgaaaagc ggttgcatgt atggtgccac tttggctttc tcatcgccgg caggaatccc 1140 aagtoottat tggocaatga gaogatgggo ogtgoagoag gatttgtttg taggaotgtt 1200 cetgactgag agetgetgee agageageaa tgttttgeee gtace 1245

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 497 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...497
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

aaggatgatg	gaaatatttc	attttcataa	tagctgtcgg	attagtattt	gcatattgtt	60
gcactacgtc	ccaaggggtg	acggatacga	gtacattggg	tttgctccac	gcaggtctat	120
gragarattg	agcattttgc	ctatgacggt	atgaatggta	ctccatccga	acctatacta	180
acacteagea	attettteeg	tatgcataga	gtttgagatg	cagaggagta	gtatcaagtg	240
Lyggaaaact	ctgaagatgg	gagaaatgaa	atccccgttt	tgtatctgtc	cqtcqqacqq	300
cattggacgg	cattgccgat	gageteggee	aggccggtat	aaggtcggga	gtttctccca	360
aaaggatgtc	ggcatagtct	ggcagttgtc	tgggccatta	gctttccagc	cactettgat	420
ayccegegta	tgatgatatg	tectgtgeee	gtaccggcgg	tagatatcga	caggtttggt	480
ctggaccctg	tcgatag					497

- (2) INFORMATION FOR SEQ ID NO:486
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...508
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486

gggcgtttac cactaatc	ag aaaacaaatt	cattggcttt	ttcttacgtg	aactgacgtt	60
attttaagg tcaacgta	at ccattgaggg	atatoottaa	tggaaaagcg	caatttttaa	120
ttcccctcg tattcaga	ac coactgages	aatdaaccca	caacaactga	taagcatgca	180
ttcccctcg tattcaga	ag aaactegteg	t	anatagataa	ctactotaaa	240
atttaatgc gtcagcct	ag ggaatatgta	acteggeacy	gneceggeaa	ctaotyouan	300
caaccaggca gacaaatt	tt aactatcgag	gttaagcgtg	cagegatgae	ataaggeact	360
agtactacca aataaaac	aa togagacato	gctctactaa	taattcctgt	caaactttat	
ggacagaatt gactatca	aa ccctacaaaa	aaacatctct	gaatttggaa	aatatcgaaa	420
atttatgatt taagtccg	ca taacttacat	cgaactcacc	ttatgagacc	tttgaaaaat	480
		cgaactear	· · · · · ·	•	508
aaggagatgg gggaaaag	ga gaaagcaa				

- (2) INFORMATION FOR SEQ ID NO:487
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...412
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

tgacagacgt tccggtaagg	tatecaaace	cacaccacaa	gctaccgaga	agaggataag	60
tgacagacge ceeggeaagg	anatagtatt	tetteaatac	agatatotot	gacggcaagg	120
gttgaagtcg aaccagaaga	Caacygcacc	ccccggcgc	~~t~ataatt	CCGCGBBGBB	180
aaagtatagc tcccaagggg	catgctgaaa	gccggatgag	ggtgeteatt	ccycyaayaa	100

aacctataaa	atacagtcct	gtcttccacg	acqaaqctca	aaaataaaaa	taagcgattg	2.40
aaaggtacaa	ggtggtcatt	uaacaacaa	agatast	-t-t-t-t-t-t-t-t-t-t-t-t-t-t-t-t-t-t-t	caagegatig	240
ttcagcgagg	2572370000	5 aucaacyay	geggtegatt	cttttatctt	acagageggt	300
tetagegagg	acyaggeteg	teacettegg	aaaaaagtca	ggaaaagttt	ccctgatgct	360
tatategtgg	tttatgaagc	gggcaaacgt	gtgagagaga	tatattqaaa	tt	412

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...5\overline{22}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:488

Sacratage condition of the same and the same at	t a c g	eggetegga agaegeeet agtteteta egetgeate tageaaege egageaagg	tacttaggag ttcatccgca agttggaaga gaaaagggct ttacgcagat ctgctgcatc	cagatettate cagatecteg taceaageag agtaatggta getattacea egecaacete egeaageget	gettgtegee ctttgeegaa gtegaacagg cettgteeat ttggaetgtt taggaggteg ecaaaccett	aatcettacg ggettegetg aagaggegga tgtgtacage cagtcategt tgteggeagt	attattgcgc tcatggcatc	60 120 180 240 300 360 420 480
5, 3, 1, 2, 3, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 3, 1, 2, 3, 3, 1, 2, 3, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3, 3, 1, 2, 3, 3, 3, 1, 2, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3,	_	ogugeuugg	cegeegeate	cycaagcgct	ccaaaccctt	ctctgccgct	tccagagctt	480 522

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...601
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:489

		ttcaatgggg	acqatcagct	acageceaca	tagtcgatac	60
ttgcagaagt	gateageeat	Lucaaugggg	9090000900	acttttcaaa	autasaggg	, 120
gcgcagggaa	tttttcgacc	atcagcagca	ggtgtetteg	actitiogga	9909449999	180
caddadadd	tcaagcgcgc	cctcgaatgg	cggccgcagg	cggacacaat	Cigaccacgg	
taggagaagg	caacsaaaaas	aatccatgat	ggctaagcga	atgcccggaa	ttcttcctcc	240
Legggagtee	cggcaggga		aaratatact	contraccad	taagtgggag	300
gtttaactta	gegaateget	cgaaacgacc	aagacacacc		totottocac	360
tcaattcgat	gctcctgacc	caacgccctt	teegntegee	ccacattcca	Cocceege	
aggactcata	aataacaaca	cttatccaca	qccggagaga	tcangtctgg	cgcacaatgg	420
ggcaccegeg	55555555	tgccgagttc	aaccactcca	ttctcgaggt	gatgcggcag	480
cgtgctcttt	ttggatgage	cyccyayccc		tascaataas	ttatcctgcg	540
cctttggaag	toggcagato	accgttttcg	agagecayaa	cyacygraya	ttatcctgcg	600
gattcatgct	cataactacc	attgaattcc	tgtccttgcg	gctactacac	cattccacac	
_	- 9 - 9 5 - 9	•				601
a						

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 536 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...536
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490

ogot aggaga	aaacaatccc	atctccgagg	gtaccctgcg	gattggtggt	cttcggtaga	60
agacagcaga	tagagagata	accetcacca	tatgcttgca	tagaaaacga	cttcacgccc	120
tggcagccga	teeeeeggtg	gecaceaeeg	annagangan	catctatcag	caattcgacc	180
atgtccccaa	teceatgtae	graegeeegg	caacegagge	geogrates	caattcgacc	240
gcttggtgat	tgacaatatc	tctattgcag	aagtttgcag	-tt-	actatataca	300
tegtggcate	ctaccggtag	aatcaccccc	tgcatgcaga	ateegettyt	ggtgtgtccg	360
ccttcaagec	ccagagccaa	taggccatca	gcttccgtat	cgaacgcatc	eeeeaacyya	
tcaactcatc	gatecgetee	ggagcctctt	cgcaagtacc	cttacggctt	Catectcaca	420
	cctacttcaa	catatcatta	tagtgggttg	teceggtgea	tegteageag	480
aayyeeeeya	terestass	attataces	gtacgaattg	ctctcatqqq	atgtca	536
caggtaaccg	tgegaeteee	Citytycada	geacgaaceg		-	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 641 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{41}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491

gacgtcatgt	cagcgaatcg	atacaggaaa	gcccggaatg	tattttaaa		
tacttacata	agaggatagt		goodgaacg	caccicigae	caagtegata	60
ogoccacacg	agaggatact	arggictatt	gatggaagtg	ctatctgctc	tgtgtcggat	120
ggcaggttcg	gggagaggga	ggttccggcg	agctgtaaaa	Cogatagata	agattataga	
acggcatttt	ccaaaaattt	Cattetenat		Jogacagacg	agactgtege	180
0+000	·	cattyteaat	tgactgnttt	tcaagtggct	ggatatagat	240
acaaaagtat	caaaagtaac	cgatacaggc	tatggttcgg	aggaaaactg	ccattgatac	300
agcagataga	ctgagagact	totatoaato	ctcaatctta	~~~~	courtgatac	
+00000000+		og ou coudic	Cicaatotta	geegatttge	ttegaegtet	360
ccyaaaagct	aataaagtag	ggtttccatg	ataagccggt	tgcctaaccg	actotaagga	420
gcaaagaaag	agggctgtga	caaaccgaat	tttgacacag	0000+++++		
aataccccaa	taattaaaa		ceegucacag	CCCCCCCCCCC	ttggaatgcc	480
aucacccgac	caaccaaaaa	caaggcatcc	aattctttct	tgaatacgtc	tttggactgg	540
cacccacgag	cttctttacc	acttcgcccg	ttcttgatga	acaaaatata	aaastatta	
gcacgccata	cttcetaaaa	39++		·	gggatattac	600
J = = 3 3 3 4 5 4		aacceegtat	ttgcatcaca	τ		641

- (2) INFORMATION FOR SEQ ID NO:492
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1137
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492

atgettettt acaagaggga ggtgateatg geatteagae eeaeggattt eeettgteeg 1080 tageacetge tateatgagg tgaggeatet ttgeaaaggt egaagataae aettegt 1137

(2) INFORMATION FOR SEQ ID NO:493

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 900 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:

900

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...900
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:493

aacgggggag agactetget eeggeagatg ggeggeeaaa gaggeggeaa gteggaageg 60 120 attegeteca egaggetete ttegeetget etgaacteat tegtateage eggetaaaag gtgggaagaa aagcatttgc ctttcctcaa ttgttttccg ataaaagcct tataatcacc 180 ttetegeaat aaateegaaa ggagttggee ggattgtteg tttgtatgta tagaegggag 240 getecetect aageatgage tgatagagta getgataage tegttegtag gegegaaate 300 egggaaacce aatatgetgt ecagetgggt gaeggetaca agactacatg ttegttatag 360 acttgcccct tgatcagttg cgtgccaaca agatatccac ctctttcgct tccagacgcg 420 ccagagette gtecatette gteggeteat ggecatateg etgtecatte tgaggataga 480 gacggtgggg aacgtctttt aagctcttcc tctattcttt cggctccata ccccacaggt 540 gcaggetget eggeteteet aegecegatg eeegettgea ggagggaega tgegeggaag 600 gggtctgctg tagccgcagt agtggcagac gagcataagg aatgcttgtg ataggtgaga 660 ctcacatcgc agtggatgca acggagtttt ccccacaaga gctacaaatg atatacggag 720 cgaagcccct tegatttgga ggacgacggc cattttttt tgccgaatcg tetetteaat 780 840 agctagacga gggggaaaga aagcagttca cctgcaccga cctgtctttg acgcgcatct tgcccatgtc tatgacttcc aaatcgaatc gggggcgaac ccatcgtccg gccaggtgat

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION $1...1\overline{1}21$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494

cagetegatg gteageatge ggeeatagae ggatatttte ggetgtttnt etgtggtgge nagacgatca ccgtctcgtt ttgtttcaat atctggatgc ttcatcgaat aggagggaga 60 tettattgcc tgtttgcttc gtgctaccat tgccggcgta gccttnagca aacgcggggg 120 cgtcacatca taaggccccc ctccggcgta cccatattgg cacatgccga gagcatccac 180 240 aagccataat gacagctgcc acnacggcaa gctgcaatcg gccgaaacgg ttcttctcat 300 aaccetaaga aatataggtg ctttggccac aaaaatactg tttcgaccga tacttctccc 360 tetgecaaaa geceetege ggteteetee geeegaegeg ceacaggaag aaggaacaaa acctettgcg cggttttact cttgacgaac aatacaaaag cattgcagec atcteteete 420 getetgeatt tegteegtga aaattattgt ttgetattee taaaaaegtg gegegaaaaa 480 tttccgctct cgcgcgagat tttttcaaaa cccgaaccaa aacgaaaaat tttggcgcga 540 600 ctttttcaag attgcggcgc gactttccgg cgatttcggc tcgagatttg ttgttcttct tttgtctaca atctttctta tggtgttctt ttgctccctg caaagaacgc aaggccgcta 660 tttgtgagat ttttttcgtt tttcttgctt ttccgggctt gttagataac tttgccctca 720 780 aatattattg tgtgagttat gttggtcaac ttcactttta agaatttccg ctcttcagag atgaaaaaac tttgagcatg gaagcttctg ccatcaaaga acttccaaat ctgtcattag 840 gaaaggaget tacaaactee tteeggeage ettttataeg gageeaatte aagtggaaaa 900 agcaatgete tttttgettt gecaaaatge gtageategt attggatteg gtaaaattga 960 acceteaggt acttettteg tttegacece gtttatgttt ggaategggg aatetgeeaa 1020 aaaccaactt ctttttggaa ataccaattt ttgaaaagac g 1080 1121

(2) INFORMATION FOR SEQ ID NO:495

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 624 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...624
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:495

gggcagaaca ttgcgcagca gaagacaggc tttcctaggc aggnngaagc actacgccga 60 cggctctgca cattagcatc ctcctgcttc accaagattg tccatccgag cctacgaaaa caagettgte etegaagaaa teeagatgae eeetgteatg ateggeegge gttegteetg 120 180 actggtagca aagagctagc cgaaaggcca ctgagcaagg cttccgccgg aacgatagaa 240 acgatgette gggagacaaa gaagetgeea eeggataggt egaaacatee tgtacacaaa 300 actgtaatgc ccgttgctgt atgctatttc agcggctttg gttccatatt tatctcaaaa gagategget gategggeaa ttettteagt ggteaagtaa gateeteteg ggaaeggega 360 aagaaccgtt ttcgcccct agttgttcac ggtaagttcc gtactcatcc gattggccat 420 atoggoagog taagaogtaa tigatotooo toaagotoga aaagtacaga otocaaaatg 480 gaaagtgtac tgcgtgaage tatgacgcgg gcaatcaatt gcaagtgtgc aacagggacg 540 600 ttgttggcta cttcaacttc atgg 624

310 (2) INFORMATION FOR SEQ ID NO:496 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 489 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...489 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:496 cgctcacgct cggctatacc ccctcgccca tgaagcagct taagctggct ataacttccg 60 aatccaacgt cetgcaatcg gecaactgaa teeetacege tacagaccaa egattatcaa 120 gtacagtatg gtaatcccga cctaaagcgg agaagcgtca ccacgtcggt ctctcctata 180 atcaatacgg agccaagtca tgcttacagc atcgctcgac tacgacttct gcaacaacgc 240 cateegaatt acacettete egaceeggee aateeeaate tgtteeacea gaceatggea 300 atateggaeg agageattet tteagettga atacetatge cattacaege eggeegtatg 360 420 ggtcaggatt atgctcaacg gaaatatcga tccacattcc aaaagagcga agcactcggc attgatgtca attcatggtc cgcatggtat actcangect gatgttcacc ctgccgaaag 480 489 gattggact (2) INFORMATION FOR SEQ ID NO:497 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 366 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...366 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:497 60 gttgaatgta nagactgaat tcggccgatt cttcggattc gaaacgctgc ggctttctat

ttcgacaacg aactcatcga aaaaagcttg ctcacagcga tgaattgaag tggtacaatg

actaccagca gtgggtgtac aagacgctgc tcccgaactg actaccgagg aaagagcttg

gctcaaagag aaaacttgac tatctaacca caaaaatggc attaatacag agtgttaggg

120

180

240

311	
gettteeeet ataateggeg aggataeett eetegeegaa aatgeeaeta ttgtggegat gtagteatgg geaaaggetg tagtgtgtgg tteaatgeee gtatgegagg egatgteaat teeatt	300 360 , 366
(2) INFORMATION FOR SEQ ID NO:498	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 468 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS</pre>	
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1468</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498	
ggcaggtcga gatacgagtc ggggccggce accacatcca cgtgatgttg cggatcaact cctccttgac gcgctcggcc atgcagcca ataccccgta acgagacggg aagaagcccg tcttttcttt	60 120 180 240 300 360 420 468
(2) INFORMATION FOR SEQ ID NO:499	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 545 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: UNKNOWN	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS	

(A) NAME/KEY: misc_feature
(B) LOCATION 1...545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499

(ix) FEATURE:

atttqtaqca	ggagtgcata	cgaagctatg	ttgaacggat	gcccagaaaa	gaatcggcac	120
tgcgctgata	gagttgcagg	ctcaqccqcc	gtcagcgaca	tagaactgca	tgaaacagtg	180
gcatagaagc	agatgctatc	ggcaagctgg	cctacattcc	acgagcatac	gataatgcgc	240
caacttccaa	ttettegege	agetggegea	gcacctcctg	catttggtct	atatecetee	300
ccastaatcc	aaccaactac	gccactggta	gccatatata	qgtccaaatc	gccgttctca	360
tcagcccatt	cattccaaat	gegtaegeea	tgtcctgcag	gtaatgcacg	ttcgtgtcac	420
			ggacttcaag			480
			atctgatggc			540
taccc	2222200	<i>y</i>	3 3	, ,		545

- (2) INFORMATION FOR SEQ ID NO:500
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 - (ix) FEATURE:

480

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...480
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:500

ggcacggtgg gtgctgcgat ggaaggatgt gtgtgtgatg tgccggctcg gccgtttcgc 60 tggacgacca tagcgagatt tgcgatatga gtcatgcccg gcctatgccg tgcatgtcag 120 tcgtatgatc ctgaagaatg gcttgcccag gacacgatgc taagcatgaa tgttccgaag ggaaaacctt tggggcaaag ccttgcgccg ttacggacgg tcgttttgtc gacgaataca tggctccgaa gatgcacggg gcaatgctgt gtattggatg acaggacgtc agataataaa 300 ggcaccatag agggtgattt ggaactgatg catgcgggct acgtacacta tctcccatca aactgaatat gacttcgaga cgttatctac cttcttggag gaacttctca agaggagccg tctgatctc tctcccctt cctgatttc tttattgcgt atgcgctatt tcatcgtagc

- (2) INFORMATION FOR SEQ ID NO:501
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: UNKNOWN
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION $1...4\overline{37}$

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501

(2) INFORMATION FOR SEQ ID NO:502

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 617 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION $1...6\overline{17}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:502

geteggtace	CCCaaaacat	tagastasas				
222222		cygcacgaga	acgcccctgc	ggacaaagac	acactcatag	60
egaaccgacc	cycycageca	aaaccttcta	cctatccata	cggaacttcg	actcaaccac	120
agatattctc	tctgcgaaga	gtgccacatc	cccatcacat	Costatata	ctattctctt	
taccataacc	gatctatget	303000		ccatgtatee	CLATTETETT	180
~~~*	- til	acaceegace	gatgatettt	cggccgatcc	cgaatacgga	240
gaatactegt	CLLLTTATACA	ccctccgaag	caagaccatc	ccatagetta	caaacaataa	300
tttcatcttt	tcctgaatct	gettgegeat	tettengege	gacgaaggat		
agtccccatt	totttottt	2022444	torraggage	gacgaaggat	cgntcccatt	360
2		yayyetgteg	taggcagatc	tegtgetgtg	tgctttcagc	420
acceguageg	accongrace	tccatactac	acqcgacctc	tegeeteagg	ctaaccacc	480
atccttttcq	acqqaacqqn	gaagatccgc	C828C322G	cgaaccagaa	Juaguage	
acaaatcata	aaaattaaa	anaga cocyc	caaacaaca	cgaaccagaa	atcatcaaat	540
	addattegaa	aacacgtgcc	aaaaaatttt	cgtttacggc	gtaaaaattt	600
ctttccggtt	cgagaaa			-	-	
						617

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 456 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...456
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:503

ttggatctac cctctatt	g aagggtacac	acaacataag	actatatcta	tataaccaaa	60
ttctgttgga tctaccct	et attegaaggg	tacacacact	caagggtcgg	gttcttgacc	120
ttacctccag ttggatct	ac cetetatega	agggtacaca	caactataaa	ggtttgttca	180
aggaatgtgc taccgtgg	at ctaccatcta	ttcgaagggt	acacacaacq	atqcqqacaa	240
cgtcctgtac tccgtctt	at tractetora	ctctattcga	anggtacaca	caacatcaat	300
egtectgtae teegtett	gt tggatetace	etecatecga	ttcaagggta	cacacaacat	360
tagetegtee geegacae	gt cttgttggal	Clacecteta	tetaaaaatt	cttcctcatt	420
gattettgat tggtgget	tg ggcgttggaa	attgcagtag	Lglggggall	cttcctcgcc	456
ggggcttttt cgctaaat	tt gaggeggaeg	aggtgc			430

- (2) INFORMATION FOR SEQ ID NO:504
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 712 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...712
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:504

cttgatggat tactctaaaa atagcatcca ggcgggtata gaacaagaag tttacgcgcc tataacgagg	agttctattc gctgtaatta tcgttcgagg aaatacgaac tttttcgttg acgtttttcg tgtgccttat tttcaggtat	gcatgtggtt atacgtattt aattttgcga cgaaaatgct tggcgcgaga ggggcgcaga cctttatgtg ttcatcttgt	attttttatt caagagaagt aacctttaac gaatagagaa	tatatttaat tttgcgagga gaaaatagaa tgcgtgtttt tctgaaccaa cggttcgtga aagagatcaa gggataatat	aatcggatat aaggggcgag ctgaaaaccg aacgaaaaag atgaaccggg gacagccgta cctctttcga	60 120 180 240 300 360 420 480 540
tataacgagg gcaagtctgt gtattgggta tcggttttga	tgtgccttat tttcaggtat agtgggcgat gataatgtta	cctttatgtg ttcatcttgt tcgaggaggt gcgagacccg	aacctttaac gaatagagaa tcgatcataa	gggataatat gctcctatat tcatgaataa	cctctttcga tagagatact aaggtttatc	540

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 450 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...4\overline{50}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:505

- (2) INFORMATION FOR SEQ ID NO:506
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 482 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...482
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:506

ggacaaaatc	atggagatta	tcatgagga	acatataccc	ateataataa	gtcagccggt	
agtccaaagg	tataasasaa	2022	·	geageggeae	greageeggt	60
·	cycygacage	Caagttgaaa	gctgccggag	caaggtgata	catgtagtga	120
gcagtgccac	attegetege	aaatcagggc	agccaatata	anagaata.	<u></u>	
attenaance	~~~~~~		agooggegea	gacgccatcg	tggccgaagg	180
Jerryaugue	ggcggaacaa	Lygacgagag	gagactacga	ccctctattt	gatacctgaa	240
gtagtgatgc	tqtqaacatt	cctataatta	ctaccaasaa	~~+++	y_uucuuguu	
tacaaataat	**		cegeeggagg	garractee	ggcctgcagt	300
- googe ege c	ctggctttgg	grgccgarge	ccqtacaaqt	gggacccatt	ttactatasa	360
tgaggaaagt	teggegeata	aagactttaa	ggegettgg		·	300
atamat		augueeeeaa	ggacattgcc	cgccggtcgg	tggaagggag	420
acachatget	ttcgctcaag	gttgtatcgn	ctacgcgact	gctgaagaag	aaattotato	400
		-	J - J	J J Gude	uddecetate	480

(	(2)	INFORMATION	FOR	SEQ	ID	NO:507

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 497 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...497
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

	L-L	accatasaaa	ccaaggagct	gatcgacaga	ctacacccac	60
atccggaatc	tategaacag	gecatgaagg	ccaaggage	togaaatoga	tetteatgee	120
gccggcccga	aagacttcta	cagagaaaaa	accyaacaaa	tetattagaa	tetteatgee	180
ggcgaactac	tcgaaacgac	ggcagggtga	agaatgggga	tatattycay	taccaactgg	240
acasattees	caaaatataa	aacaatacqc	ctcctgtaag	ggacaaaaga	0050	
++	atassacat.	attacaacaa	gcaatagaaa	aayaactgcg	cacogoraca	300
teatycaaay	gradaggede	gootoottoo	gagaatatgg	tttggtgcta	cgatggtgat	360
aacaacatcg	tttteaggat	geeteetee	gagaaaaa	agaaagaaaa	ttcctggtct	420
cattcattga	aggatagtac	cagttcctgc	cyatyyaaat	-++-+-	tteetggtet	480
taaatgacga	tttcaaagcc	aggctacggc	ggtacacaac	attatacaag	cttatctcgt	497
ggctgatgaa						401

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 403 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...403
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:508

geeggtette eggeacgaga ggeagteege tgatgetege catttegata aageegtetg teegteageg gatataceat aagaageete gegeatttea ttagtgggga gtgtgeaega

60

120

acg	gctatgc	gctgcccatc	tgtggcacta	tcagtacatc	ctgcatecee	tctcccccat	180
cag	Jetaeggg	cagtacatta	cttctgcaat	cggacaggct	gcccgtacgc	cctcagcagc	240
tge	cttcctg	cctcgacaga	ggagagacaa	cccttgaagg	agtetatoge	tatccgatct	300
tet	tcattcc	gcatttagtt	tacaacaaaa	tccnggaagc	actnaagcat	tccaaacaaa	360
aat	ttcaaaa	acccaagaag	aaaaaacga	taacaaacta	aac		403

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 517 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...5\overline{17}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509

aatttttatc aatcgaatta aaagtgtgtc cacttatttg tattaaattg gccttaactc 60 taaaaacaat gaactaggcc aatcttttta cctcatttcc cataaatgga ggcaaagaga 120 gettetteee ttegggatgt teattgettt tgatagaata atatatgtgt tagagattte 180 caaggtctat gccacaatgt aattcgatca ttttatagat tgctcataaa aaaatattaa 240 gtgtaggaag ctgaaactta cagtaggcat atctttattt ttccttttca gtggattaca 300 tcgaaaagag agggtatgct tcatataacg agaggacaga tataagaagt ttgataaact 360 gttttcggca gtcaagtcct ctcaaaaggc aaacttcgag ataggagctt cggaagaacg 420 ctacaatgaa tcacctattt tatccttttg cccgaagage cctcttegga acgaaagaaa 480 accetteggt taccactatg aattgagega ccccaag 517

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2313 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...2313

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:510

agcagagaaa 8	aatccgcat	cgggccaatg	agattcactt	ctcatgccgc	aggctgaagc	, 60
agtaggatta (	pospetaner	aagtggcacc	tgcctcttca	actacycyac	Caaaacaage	120
agagagater 1	totoogooga	addcdataad	ccaccatage	agecucaggee	~~~~	180
+++aa+++ac (	caatteacet.	ttacagaagg	agcctccyta	cyaycayyay	agegouses	240
aggagateta i	ccaaaaatct	accadatada	qatcccgtaa	Ccaaggcaaa	gattottatg	300
aatcggctca	Seaggagagagagagagagagagagagagagagagagaga	caacaaacta	aaaagctqqt	aaagatcaga	tcatttcgaa	360
caaggaatac	gaacagactt	acaaaaacta	togacagoca	agaccatata	cgaagcccaa	420
gcatccggca	ccaatacaaa	agggtcagcg	tageatetee	tatgagcgga	tatatcaaaa	480
nagagataat	aaccadddcd	aatacqtatc	cqtaqqccaa	Cocatagoca	ccgcgccaca	540
aaccgccggt	taceagggeg	aacaaaaata	toggagagee	atttcaagat	gtccgcaatg	600
totooggtgo	cascttccag	acttcatacq	acaacaactc	tacgagetgt	ccgatctgaa	660
cggaaggctg	ctateattea	agcatgatee	acacagtcat	cctacatccc	cgttacattc	720
eggaaggerg	atatageast	atcataccca	actettteat	cactgtgtat	ctgctctcca	780
gaattegaca	acgeggegae	ccattcccat	atcooccatt	accgaagagc	aggattgcac	840
ataccaggaa	taagettaa	casaasaasa	tatcagaaac	aaaggttacc	ctcgggcaga	900
ttegtetate	tactatacas	atcctatcca	actgaaagcc	ggagacaatg	ttgtgactca	960
gcaacggacg	cogcgcgcga	according	tegtecgtaa	tgcctgaagg	tcatactcac	1020
tggagtatat	caygugaaac	catoctoaac	aagatcattc	ggttetetet	gaacaaccgc	1080
taaagagagg	gatactegat	atactactaa	tactaatcaa	cacctatogg	cctccaatat	1140
tgaccatatt	ggtageatee	acttanacc	tectacatea	tagtgatgac	ggaggntacc	1200
ggaggtggac	gtatteecty	accegaacge	taaccttccc	catcaagaca	gccgtcaatg	1260
ggtatggcac	ccgaggaagc	tagastagta	ttccactaca	ggcttctcta	tegtttgggt	1320
gagctaccga	egregeregeg	tattataat	acteateaga	tegtategga	aagctggcca	1380
ggattegaet	gggggacgga	gagaatgtgg	gcaaacctac	atcagecece	aatcctccat	1440
tggtcggtgc	egatetgeeg	taggagttag	gccgacagca	cctctctcca	agacctccgt	1500
cctcggcgaa	gteatgatta	agtagagagt	tactetegat	cagaaatata	gcacaggtga	1560
actttggccg	actggacgac	aggaetatca	gatactgctc	aatcccgaaa	ggatgaacac	1620
cagtactcga	ggegacacca	aggaacacca	accatcaacc	aaatgaccgc	aatgcatcgg	1680
tacggtatca	egetggeega	agcaegegee	atatetttae	ggactcctct	catgctcgaa	1740
gtggcgtact	gracyaacac	cactataaaa	agtotogato	atattcccat	catgetegaa	1800
tgctgccgca	cigggcaaga	aggestasag	. caccgaagtt	gageettget	tccgagcgag	1860
agegtggeag	aggaagggcg	ggcaacaagg	acadecade	acgagtacac	tgagetgace	1920
gaaatctgcc	gtactcgtga	ggaggatata	. deageegge	ccctccgat	gtgaaagtga	1980
gaaaggttgg	ategetetet	ggeegateeg	caaaaattct	atcagcaaco	gtgaaagtga tacqaaaagc	2040
gtacagacat	atteegteaa	gagegeeee	. cguadacto	attttcctg	tacgaaaagc	2100
tetgtacgaa	ggaggcattt	tegegetea	cgtattact	dttgcatcct	tgaatgctcg	2160
tgccacgatc	atttegetgg	LCaccatte	, actatagae	gtatectate	ttttgaactc	2220
aaactgatgg	gactgaccat	. caatacgatg	, agicicggas	a acacetaca	gccatcggtc gaaaccgtat	2280
gctggtggac	gatgecateg	ggaegraga	aacyacacac		gaaaccgtat	2313
gaagcctgcg	aagaacagga	cacgtgctca	acy			

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 390 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature

### (B) LOCATION 1...390

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

gaaattgaca gaaccgtagg ctctatgtte etegaategg ggatgttett aaag teettagggt getegaggat gaaaageeeg tettetgeag tatgttaett teta geggtggeat aetttgtgen teeagaaat eagtttettn gtteagatge ttaatgaggt tgegantaaa ggetgeatge teae teetatggaa gtgaeggaag aacaaceeeg agataetaat teeatgetat aete eegganaata ggtegatage egaaagteet	atactt 120 gtcata 180 ctccag 240
------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------	----------------------------------------

# (2) INFORMATION FOR SEQ ID NO:512

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 483 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...4\overline{83}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:512

gcacgtcggt cagcacctcc acgggagtat gcggattgag cgtgacgccg atttcatgcc ggccttgcga atcgccgcca gtgagcgatg caggtgcgac tggcttcata gtggacgttc 60 atcatataaa cgcccagttc ggccaactgt ccacgaactt catcggctcc acgatcatca 120 ggtgaacatc gagcggttet tgcaaatcgg teggatagee tegagaatgg gaaaacegaa 180 cgaaaattgg ggacgaatac gccatccatg acgtcgatat gcagccagtc ggcccgctgc 240 gattgatcat ttcgacatcg tcggccagat gcangaagtc ggngacagca aagannggag 300 atacgatagg ttgcataagt atagtatcgg gttatttttt attgattcga tgctcgcaaa 360 gttatgcctt tcttgcgcga tccctgtaat tttcagacgg gctatcctat ggtttaccaa 420 aat 480 483

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 581 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...581
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:513

aacctgtggt tttctcttcc cgacagacag aacagatctt ccggtcatca aacagctgca	aacggcagat gaggcactgc agcaagattc caggacatca cacttgccac gggcgacccc	gatgeegaca gageaaccet gtgeagatac ataaatgtgt caaacgeegg gteaccetgt acttacactg gtcaatggaa	cccgtcacag tcgatcgaat caatcgccat cacgtgagtt acgcactatc aagcaggatg cactcggcat	tggagetgae cegateggge taegageege acacaatgag gaaggegatt cteaggtgat agtageeggt	tatcagettg accecttett caaggtgtat aggettaceg egaagaegaa eggeaattgg tteeeteete attegtetee ttegateaga	60 120 180 240 300 360 420 480 540
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# (2) INFORMATION FOR SEQ ID NO:514

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 525 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...525
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:514

ggacaaggtg gtggagaato ttggatcata cgctgctgca tagccaatga gcttggcgtg tgatttggcc ggactctcac caccgctgag ccctgtagtg tataatgctg gacaagggac	gggcctccg gggcttagat ttcgttggaa gaagaatatc	cactteeggt tecaacgatg tetactegge etecatteag	cccgtcctcg tacttttcat catggaggac atcatctctc cctttgcgcc	acaagccggg agacgaaata tacctataga cccttcacc cgtttcggga	60 120 180 240 300 360 420
tataatgctg gacaagggad cttgtgggag ctactactcg tcaatcttca tctggagtat acgcattctg aggtgtcctg	cagegegey cageggtttg tegatgtgea	ctacggcacc tactattacc	cctttgcgcc ggtatngtgg	cgtttcggga	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 564 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...564
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

atcgccggcg tccgggatag tgccttgcgc gacaatatga cctgcctcac tccgaaagtt 60 tggcccggaa gatgggggc gatgtcctgg gcaaacggtg cgaccggcag aaagcaaatc 120 ggaccgagcc atcacgatcg gaggtgtttc gaggatctgc cccacaacag cagcatccaa 180 gccgatatgc tcctgccatt acgtggatgc cggccgagag cctgaacaac tggatcggca 240 acgacgctac atagcctacg teegtetgeg teeeggtgtg tegeeegaga geetgacgaa 300 gctctcctgg agatgcaaaa gcggcatcag gatatggaag tctccgcaaa gcaggagtgg 360 aattgcacta ttcccttacg cccttcaacc gctgcgtctg gaagatccca ctttggtcaa 420 tatgctgcga atccagcaga tgtggccata gcggtgctgc ttatttcgct gctgaactac 480 gtactcatga cctcgccttc atggtcaacc gccggcgtgt agctgccatt cgcaagtgta 540 ctggagccat gcccgtgcag atac 564

- (2) INFORMATION FOR SEQ ID NO:516
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1405 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...1405
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:516

agggtatatg tataaatagg catgtgctta ntgctctcct ttcgggtatt tgatgccacg 60 attgaateet teggeeagag agateagegt ttetgtagga egataceggg gatttettgg 120 atggtcgaat tcaagatgtc catcaggggt cattgtcgat ggcgaagagc ttgatcagca 180 aagagtaggg teetgtgtat agtgacaete caegateteg ggaatgttgt acagatgggg 240 gagtaateet tgtacatega ggetttetee agaegaaege etaegtaagt acatttetga 300 aacccaaaga cttcgggttg atacgatagc ccgaacctgt aatactccca tttcgatcat 360 tetttgtaeg egetggtgaa eggeageaeg egtaegeege attettetge aacatetttg 420 aacggcatac gggcattatt gagataatgc tcaggattcg cctgtcgagt ttgtctaacc 480 tttccatata tataatggct aaaaactgaa acaaatgtat gaaaaaactt atgtcgggtt 540 attttcgatt accttgagac tttatactat aaagccccaa gggttttagt ataaacgcag 600 gagactttat agtataaagc cataggggtt ttaagtaaaa gtatggaggg tttatagtat 660 aaagtoogtg gaottttaag tataatooaa ggaacatogt gttotgotta taaacgatag 720

gttcgaatta	ttqcaaacaa	gcatgcaact	caatgggata	aagggaaatg	ccatatattt	780
gcaggettaa	aatccaqcaa	attataatcg	gttttttata	tggaaacaac	ccactctctc	840
cactecgaaa	aagcatcgta	ggcgtacagt	teetetttgt	tgtttcggag	ctactgtttt	, 900
agtgccctc	cttgtgggtt	tagacccttc	gcagccctgt	ttacggccgg	catcggtaca	960
ttgatttttc	atttggtgac	aaaggaaagg	tgcctatttt	tcttggtagt	agttttgcct	1020
ttatcgctct	attatcaagg	ctacggagat	gtatgggctg	cccggtgctc	tttcgggttg	1080
atcaatataa	cattggttta	ttatctgatg	agtgctttgg	tcaagtgcag	ggagtacgtg	1140
tgatccaacg	tttqttcccq	cctgtagtca	teggeetgte	attatcctga	tcggactttc	1200
gettgeegga	gccggagtgg	atatgcacaa	tccaactgga	tactggctac	tatatcgctt	1260
getacegeeg	tgctgtaact	atgctggcca	aggggctttt	caagctgatt	cccatcttct	1320
gcgtatagtg	gtaggetatg	tgaatagccc	gtggtttcta	tganggcgat	ctaatcctgt	1380
	tgcgtggttg					1405

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 548 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...548
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

ataccccaaa	ancgactcgc	tcaacattcc	acggccacag	angaacacct	gcggatggcc	60
				agcagcctct		120
tgaatatatc	catcaaqaat	agtagcacat	agcatcgggt	actccgggcg	ataccatcag	180
tatcatagca	tcccaacatt	ggctctcgtg	gatacggcag	gcgtttccgt	agcacggcaa	240
acagaaactt	gtggcgcgat	gtcccgttca	ageteegtee	cgattcgctc	aatcgctgaa	300
attetteate	gatgeegget	ggcagatggg	gcagagctac	cgctacggat	cgactcggcc	360
gtctggcgaa	gegtgtaega	ccggtggaac	gccccgtgga	gcaggtgttt	tegtteette	420
cqqaqqaqqa	teteageage	cgttactgaa	gttgtcggga	gaggctgaca	gtactgccgt	480
				agaaagcaga		540
tectette	, ,,,,		•			548

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 499 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...499
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:518

getegaatgt tettgaatae ttgtteggte tgetetgtta eteegeeggt acaaagttee 60 ctgtggtagg atcaaggeet aattgteegg aageatagge atattaeeca teaggatage 120 ctggctgtat ggtccgattg cggccgggca ttcttcgtgt tgattacctt tttcattacg 180 tactgttttt tatttgatta ttaatttgat gattgcagtc tttgctgtcg cactacttcg 240 taaatacaat geeggeegea aeggagaegt teaatgagee tatageeeee ateteggaat 300 agetactatg ccateggeea tectaagegt atcaggtgat ggeegacate etcegeeee 360 atgactatac ccaaaggcag cttcatgggt actcggtata tagatctgca agccttcttn 420 cgaagcaagc gactatgcct aaccgnattc ttgcaagctt gcagatggct tccggaatgg 480 aagtcacgcg caaaccgga 499

#### (2) INFORMATION FOR SEQ ID NO:519

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1513 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1513
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519

ggccctccgc cggatttgtt ctgtccggct ttcttcttct gttcgcgttt ttcgctcgtg 60 cettacgtte tegetegegt tgacgaagtt teteettege teaegttett tttetttaag 120 ettetgeteg egiteettit gettgagegt tgateettaa gettgtegeg aegggetttt 180 tetegitett titeeetget ticaattete gittgegate gegeteettt tetegettgg 240 cettlegagt gettlettt egteettete attltgtgea egetetttgg ceagegetga 300 atctgctcta ccgagacgtc tttgccttct tgctgcttga gcgtggcaaa gcagctgcat 360 ctgagategt ateggetgeg gaagaategg etecacagge ttggeteegg agagatetge 420 tecetatega tgtegaaagt ataggagtag cegteataat getgteettt ggegggttta 480 gatgganaca gaggtttcct gtctgtgccg gacgtactat cgcgagcggt atcctcggct 540 cgttcttgtc ggacacgata ggagccggag tgccagcagg ctctatgtct catcctcttt 600 gccgacaget tgcgctcgtc cggtcatctg ctgccaggat cgaggacgaa ggccgtctcg 660 ggcacttett ettttgegag gaaggtatgt attgacetat gettttaece ttgacaagca 720 gctggtaatt gctctcgata tggggaacaa caggctgctt tcgcccatcg cactcataaa 780 teegteggag egaaageate ettgatatae tgeeageeea tgegtggggt eggagagagg 840 teateageea etgategaat geteecaegg tgetetgeae tatteeagtg tttgetetgt 900 atagcgagag aagttgaatg aagcaagagc aaaagtaccc tgtttttatt caatgtaccg 960 gcaggagcaa gaaggatcag cgggtacgct cgaaagattt gggttttaca aaaggaggca 1020 aagagteege gatatgetgt eggtateega actgeeceae egaatateee agtegatace 1080

gtatageege cetgtaega atteggtgae gtetgettt ttggagtetg actecagea eegatagggg gaatgeteg tttaggtagg agtegaaeg atteetteag ataateggg taggateaag gegeggeaa aaagagaega tag	c ggataateet c ataacgagtg c ggcattcatt c ttgcccgtag a ttgctcangg	teaceactge cattgaggaa tetgetettt agttegttet cetttgecag	ttcagggcag gtcgaatttc ctgaccgaac ggcgacgatc atgtcttcgg	agtgaagccc ggcgccagtt cgactactcc catgcggcca gatagtactg	1140 1200 1260 1320 1380 1440 1500
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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 544 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...544
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:520

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 475 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...475

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

agagagaacg	gaatcgaatc	gaccaaagtg	++a+aaaa		cagcctcaag	
atatem	January January	gaccadageg	ccccggeega	gcgagaacga	cagcctcaaq	60
occogguate	getteadat	cgtgagatcg	agettgtgte	aatatcaaca	agaatottag	120
CGCAGGAGAA	ctgaccaatg	attataaata			agaaccccac	120
J J J J	ergaccaacg	gitataactc	cgccgtgcag	ccatcgacct	gaatatcccg	180
ctggttacaa	atgetette	gettetgeet	tastasaara			100
	3	goodeageet	ccaccacgge	attetgeaaa	catageeetg	240
aggatttege	atcaagagtt	gggctgaata	caagtagteg	ctttttatta	ttgaagtgtc	
gattgtasat	+	333 . 3	auguaguag	ceceeeg	Ligaagtgtc	300
guccycaaac	ccyagagage	ctctgtaaat	ccqqtcataa	ggcgactgca	cttggaggat	200
tetettetet	ctctcctcac	tt====================================	33	Jacqua	ceegcageac	360
	ccccccac	LLCCatggag	ggaaaaaqac	qqaqqcaqtq	tntttagtat	420
ttqqacactq	cctctatctt	ttcgagggg	44	33 333-9	cugue	420
33	octyce c	cccgagegga	ttaccctnca	aaagatcaat	cccqt	475

# (2) INFORMATION FOR SEQ ID NO:522

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 463 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...4\overline{63}$

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:522

tgatcctccc	taccgtggag	ccattcaaaa	agacccttgc	castagatta	gcgatcctgt	
attaacaaaa	and not not	*	agaeceege	egacgegeeg	gegateetgt	60
	aagtactget	tecaagaget	atacgataaa	cggcagtggc	tgcacagcaa	120
gtggcagaga	agaacaaatt	tatcttcgag	acastscss	aggttotoo	ggcggagaca	
tttctttaga	anctatason	+	goguacucuu	agetteteg	ggcggagaca	180
	agecataacy	Laacacccgg	atccgtcgta	gtgacggccg	gcggtgtcaa	240
gctgaggaga	atgtcgatta	tacqqtaqac	tacctctccg	acaacatata	gateteaatg	
aagcgattct	ctcttcaaa	actoons		geddegedee	gateteaatg	300
	occeeggga	acteceatea	argreteget	cgaaaccgag	ggctgatgaa	360
Laugeagege	aaaacgatgt	toggtataga	tcgaactaca	acttttccaa	agacttcacc	420
ctcaacaana	cetteataca	ctasaaaaa	<b>h</b>	aoceccaa	agacttcace	420
ctcggcggna	ssecucyca	ccyaycgaaa	rgccgctgac	gac		463

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 645 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...645
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:523

gcctcggatt	tactcccgac	gaggaaatcg	gtcggggagt	ggatcacttg	atgtcgagcg	60
atteaatace	aagttcgctt	acacgatgga	cggcagtagg	aaggagagtt	ggagtatgag	120
aacttcaatq	caacttcaac	caaactgccg	taaacggacg	caatatccac	cccggctatg	180
ccaaqqqaaa	gatggtaatt	cgctgcaggt	agtgtgccaa	tctggcatgg	ctcttctgcc	240
cgaggtatgc	qqccqqaqqc	tactgccggc	tacgaaggat	ttttccacct	tatcgcatca	300
acqqttcqqt	agagaaagca	teggeatett	atatcatccg	cgacacgacc	gcaaactctt	360
tgaagagaag	aaagagctga	tcaaagctgc	cgagactaca	tcaaccgcaa	gtacggctcg	420
gacategtgt	cqctcgaact	caagatcagt	attacaatat	gcgagagatg	gtagagcctc	480
atcccgagat	atcqaaaaag	ccattgctgc	catgaagctt	gccggcataa	cggccanggg	540
cagectatte	geggeggtac	ggacggggcc	agactctctt	atatgggatc	ccgtgcccga	600
		aacttccacg				645
_						

- (2) INFORMATION FOR SEQ ID NO:524
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 505 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...505
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:524

						60
atacctagat	gttggatcat	gagaagtetg	tetggggtge	ttttatccta	tgacagtggt	60
gatgetettt	ggattettga	aaatggagac	ggcattcgca	ttgaaagaac	aatggggcga	120
cqqataqaat	acgtcagcaa	tatccttccg	tgagcgaaag	cgaattgggc	tctctttatt	180
cctatgatat	tatgatgatt	tgggagagga	gggaaaggcc	aagacccccg	aagcacttcg	240
tgctccgaca	geategeteg	ccatgcagag	gcatattccc	ttaccaagcg	tacccttcga	300
tattgaatat	cctcaaggat	ctgaaccaga	ccttgcacga	tgggatcagg	catactatag	360
cattecegge	gatgcggagg	aaagtggcac	cacagetect	cctatatgag	aatgcngggg	420
ggagtgaag	cccgaaagct	gatagactta	cgaataccag	accggttgct	accctgaaag	480
	accetetta					505

- (2) INFORMATION FOR SEQ ID NO:525
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 519 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...519
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:525

- (2) INFORMATION FOR SEQ ID NO:526
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 839 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...839
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

atcatgaatc tetgggtage etgteeteet cateageeaa etggetgtae eggttgtaet	ggtctacctg cattacagga gcatcgcttc aataaagttt atcatggtac tggcactaat	gcatetecte tgcetetgca aaggeteagg gageagagea gcgaaaatag etaceaegte egteeggeea	cttcttttgg actgataagt gagcttgaaa ctctgcactt ggccttgctt agtggcaaga gagttttgat	gatagtetat accetettge gtegttteee tggeaggage tactgaaatt ggteeggtgt	accggccacc cagcaccttc tcgataggat caatggtaac acggtgatct cctcccgttt aaattgtatg ttggctaatc	60 120 180 240 300 360 420 480
cggttgtact ccggtactcc aaatggttct	tcgagcagga	tatgtccatc	gagttttgat	agccaaagtc	ttggctaatc	

ttttctgctc aataagctct gtgagagcct tgatgtcatg ggttcactca ttttttcta 660 tatcttttct tgctaaatac taatgagatt atgcacacca tctcatgttg agatagacat 720 atagcatcct gcaggtttaa gcgcgaagtt caaccaacgg ccagcattcg ctcgatcgag 780 agcaagcctt ctcctgatt tcagcaggca cctttacttc ataacggntg tggggagag 839

- (2) INFORMATION FOR SEQ ID NO:527
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 473 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...473
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:527

gatttggcca	aggettatgg	cgatcaccag	gtgttttccg	gagctacatc	accatcgaaa	60
gaggcgaaaa	agtagettte	gtaggcaaaa	acggtgccgc	aaaagtacca	tggtcaagtg	120
tatcatggga	gagetgacag	actacacqqc	aagctcgaac	tggggcacaa	cgtgcagctg	180
ggctactttg	cccaaacqaa	qcccaaqaqc	taagagggga	tctcacggta	ttcgacacga	240
tagacgtgag	accatagaca	acatccgtct	gegeetgaac	gatttgctcg	gggctttctc	300
ttcaaaaaca	aagcatcqqa	aaagaaagta	agtggtcctg	agtgaggaga	acgagcacga	360
ttggctatta	tcaggctttt	gctacagccg	gcaacttcct	tattctcgat	gagccgacca	420
atcacctcga	tatgcgctcg	aaggatgtac	ttgaaaagag	gcgatcaaga	act	473

- (2) INFORMATION FOR SEQ ID NO:528
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 337 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...337
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528

gggcaacttc	ggttcggtgg	atggcgattc	gcctgctgcc	atgcgttatc	cgagtcgcgc	60
ctcagcagga	ttgccggtga	gatgcttcag	gacatagaaa	ggaaacggta	gacttccaga	120
acaatttcga	tgatacacgt	caggagctac	ggttctgccg	acacgcattc	cgaacctcct	. 180
cataaacggg	gcttccgtat	tgctgtcggt	atggctacca	atatgcctcc	ccacaatttg	240
tccgagctat	tgacggatgt	gtggcgtaca	tcgaagcaga	tggcgacata	nacgggaggg	300
cttgatgcag	tatgtctagg	ctccggattt	cccaca		333 333	337

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 450 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...450
- (xi) SEQUENCE DESCRIPTION: SEO ID NO:529

tgttgcgtta gaaaatggaa agtgcagata tggacggctt gactagggga tagctttttg 60 tctatgtagt ataagataat tcctctgtat tctgcgaatt atgacccttg tcttttgcct 120 cgtatcttgc tttcagcctt ttcaataccc ttggctatag tcttcttttt tgatgatttc 180 tagcaaacct totagacaag tttoogatto toottgagag aaaggcaatt caaattaagc 240 gtgattttat atcatcattc caagacttat ttgcactaga tattgttccg tcatcttgta 300 gctgatgcta agaaacagtg cgtcggtaaa gagattaagt gtatctcctc atccttcttg 360 gagcaatcgc aatgagcgga gccctgactc tgccactgca acatgcaacc atattgctat 420 aggatagttg ctgggcaggg ttttggctac 450

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 838 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...838

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:530

gcaaaataag	attcagcctc	ttgcaggctc	ttgtcgtctg	cttattgtta	cctcttttc	, 60
tetecaaget	caaqaqqaaq	gtatttggaa	taccctctgg	ctatccacaa	gacggaaaaa	120
gccgtagaaa	cqcccaaqaa	agtettteeg	tagccaacgg	agtactttac	tcggtgggca	180
aagaagctcc	ccatgagcaa	agatettega	ccgtatcagc	ggactcagcg	atacatcggt	240
aagcacatag	cctactccga	gcaactaaaa	tccttggtca	tatactatgc	atcagcaata	300
tcgacatctt	ggacgaagca	ggccgtgtga	ccaacgtacc	tgcttgaaag	acaatatcga	360
tctgatagac	aaaacgctca	ategeetttt	gacgtaggca	acagggctta	tttggcagga	420
ggattcggcc	teteeqttet	gatgtcgccg	aagctcgcat	accggctacc	tacgccaagg	480
gaactaaggt	accgatgtgg	ctaagttgga	caatgatcgc	ttgctgatgc	tgaaagaagg	540
cagetettea	toqqaaaaqa	gaccgataac	ctgcaagatc	cggccgcagg	acagccttgt	600
ctttgaattt	gccgatgggc	toggtcaccg	gtctgggatt	gtcggggaag	acatctgttt	660
cctactcacc	gatggccgtg	tatatgcgct	gcaaaccaat	cgtttgagcc	ggagctattg	720
ctctcttcct	ccgccattca	cgactgtatg	tgacggatcg	tggtctgttc	atctgtgccg	780
agaacgaatt	tatttcatag	aaaaaggtcg	caaaacgaca	caatttccta	tagcgacg	838

#### (2) INFORMATION FOR SEQ ID NO:531

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 405 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...405
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531

gccgatagtc	cccaqaagga	aagnngacaa	cggcaatact	cataatggca	aaaaccttga	60
ataaaaaaa	gcagaagacc	acttettatt	cttttqtqca	ttcttattgc	tatatctcan	120
anggadadag	gangactanc	acceteteen	accaacaata	gttttgatca	tcgacggatc	180
allaaayaacy	ggagaccgac	tatasttatt	taccasasaaa	CCAAAACACC	ccaatttctc	240
cgtttcaggg	gateggggee	igically i	teccaaaagg		ccaatttctc	300
cgcaaaatag	tatataatat	ggtatgcgac	tatattttet	cyaycyayaa	aaacccgcaa	360
ggtcaatccc	taagggtagt	atatattaaa	aacggagtaa	ggggctatgc	cgaanaaggc	
cggcaaaact	ctccggatgg	tttccttttt	atttgtctcc	atttg		405

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 542 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...542
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:532

ttcggctctc	tccgcgatga	ggtgagaagt	ctttttccca	attataagct	atttcgatcg	60
gttatatccg	tgaaccaagc	cgaatggccg	aactgtacgt	gctgccgatc	tctttgtaat	120
tccctcttta	gaggagaacc	tccctaaact	attatggagg	ctctctctqt	cggtacgccc	180
tgtgtggctt	tccgtgcggg	ggtataccgg	agatgatcgt	atcgggtagt	nccqqatatt	240
tagccctttt	cgtgatccgt	ccgatttggc	agaagggata	accaaqacca	ttgcctacaa	300
gaaacctccc	ccgaagetgt	tgcttcagct	tgtcgctcct	ttgtctcagg	cactactcgc	360
gtgaagtagt	atcctctcgt	atgctgcagc	tcaccgcgaa	ctgctctgac	ttgtacgaag	420
aaggaatagg	aaaacatcca	aacgcaagag	tcttttcggc	aacttttcag	cagataaata	480
tgcagccatc	ttttggcacc	aaaacaatac	ctttgtatca	taatcattat	taaqaacqac	540
tc					, ,	542

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1336 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1336
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:533

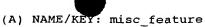
ggccatgccc cactgccacg cgtgcatcgg ggacttcacg ttgtactatc cggcgatctc 60 ttctatatta tctattcggt tgtggacgat aaagaccttc cgttgcggga catctcgaaa 120 ttgacagett eeegaacaat gteggggtga ategtgeeag tteggtggea aegggatage 180 gattcggcgg tggggtttga tattcgagag gtcgcgtgct cccatcagag agaattgcaa 240 agtacgggga taggtgtage agacatggte agegtatega cattgacetg tagttgegea 300 gcttttcttt tactgccaca ccgaatttct gttcttcatc gatacaagga ggccgaggtc 360 atggaatetg atategttge teaegageet gtegtaeeta taattatate gateegaeet 420 tetgecagat egtgeagaat cetttaatat eettggeega aegggegegg gatatgtatt 480 cgatacgcac gggaaatttt gcaatctgtc cctgaacgtc tgatagtgct gataggccat 540 acggtagtcg gcaccagtat cgctacctgt ttgccgtctg tggcggcttg aatgcggcac 600 gaacagccac ttccgtcttg ccgaaaccga catcgcccag ataagccgat ccatcggacg 660 ategetttee atateggett ttacettgee gtggeaeget eetgateggg egtatetteg 720 tacaggaaag aggeteeaat tegtggtgta ggtagetgte eggaetgaat geaaageete 780 getetettte etttgggeat agageeggat eagategega geaatateet tgaaegettt 840 ttggtcctct ctttgagctt ttgccaggct cccgtcccga gagactcagt tctacctgcg 900 catcactgtc accacctttg tatttggaca attatggagg ctgtgcagat tgacgaatat 960

				gattacatac	cacateggte	1020
tatatcgtta	tttcggtaaa	gagtttgatt	acticityce	gcccccc	cacateggte	1080
atastasaac	tecgaaccgg	ccgataccgt	gatcgatatg	cacgatatag	cogococogga	
	acctccttca	at angagaat.	cactttcccc	gaacgggttt	gtegettttg	1140
gaattggtte	ageteetee	909090999	testanogat	aaddadaccd	atccgaagag	1200
agattgtatt	tgtggtaacg	ategaaaage	LggLgacege	adgedgaeog	atccgaagag	1260
cttcgtccga	aaaaccctca	tqtaaqtqag	cgatactctt	ttcggaagga	gegaagagee	
tocacgeteg	gaaggatete	trecactete	togtattgct	tatccgaggc	tgtggccaaa	1320
		00000000				1336
agcttctgta	gccggc					

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 551 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...551
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:534

cggtttttcc agtccgtagc tcgcaaaacg aaatccaaat tctccgcaaa gtacgtccgt 60 tcagcaactg gaaatcctga aacacaatgc ccaaattctg cgcagatagg gcaactgctt 120 ccgtttcaac tttgccagat cataatcatc acgcgggcat aaccggcaga gataggcacc 180 teageataca aageeteage aaagtgetet teecegatee eactgageet ateagataga 240 cgaageteeg geggaaaggg teagatteaa attttgaaaa atgaegtttt eetetgaeag 300 360 agogtoacat ctctcatctc cactacaaga gctttatcgg ccaacttaca atatccattc 420 gttttttcag aggctatttc cgaacaaagt taaaataaac cgtggaggat agtcctaccg agtggctcag atcggtttac atttcccaaa tcataaaatc cttctttgat cagaagtctt 480 tgaagacatt tttggccatg agacattaca tattgggcaa aaaaaaagaa ttggtctacg 540 551 gcaggaccac c

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 664 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:



(B) LOCATION 1...664

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:535

gcgtcaggat	cacggcttcc	acttcgtcgc	ctacatgcag	gaagtcctgg	cagaacgcaa	60
gtgctgtgtc	catgacattt	cgcttacgtg	gataagacct	caacgccctg	tgcaatctca	120
acgaaagcac	cgtaatctgc	catcacccaa	ctttaccctt	caccttatcg	cctaccttaa	180
getegetgte	gagageteee	aaggatgagg	catcagctgt	ttgaggtccg	aagagcgata	240
cgcttcgatc	ttcatcaaag	tcgaggataa	cgacattgat	cttctgatcc	agcttacgat	300
ttcttccgga	tgagccacac	gaccccatga	aaggtcagtg	ataggataag	accatccact	360
ccaccgaggt	cgataaatac	tccgtaagaa	gtatattctt	gacgatacct	tcgagtacct	420
gcccttttc	gagettgeeg	agatttcttt	cttctgttgt	tcgagctctg	cttcgatgag	480
caccttgtgg	aaacaactac	attcttatat	tcttgattga	ttttcacaat	cttgaactca	540
teggettete	aacgaatgca	tcgtagtcgc	gaatggggcg	cacgtcgact	gtgatcccgg	600
gaggaaagcc	tcgataccga	atacatcgac	gatcatacac	ccttggtacg	acacttcaca	660
tage						664

### (2) INFORMATION FOR SEQ ID NO:536

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...931
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:536

ccaagcaaaa	ccggaatctg	tgggaatggc	acttgaccan	ccggtcggtt	cgacttcgtc	60
cgtcaggcat	cgaaggcatg	agggcaatct	ttagaccgtg	gtatcagcca	gacattggag	120
cggacgcatc	acagcattgt	gctccatgga	ctgaccagca	cgctacagcc	tgcctgcaaa	180
gageetegaa	gaatggattg	atacctgtag	tggcattatc	cgcaaaacag	atatgagccg	240
actcgataca	ccgatcaggt	cggccaaagc	atcgcgcaac	tcttctactt	ccgagtaacg	300
cgcagcgtct	ctctatcgcg	gctgcggccg	taactcccta	ccgcacatcg	tagaaatacg	360
ccaaagcctg	acgcatggca	tegggtttag	gaaagaggag	gtggcgttat	cgaaatatgt	420
attcatccgc	aatgcggcaa	ccatcaagag	caaatgggag	gtattcctcg	ctacgggaga	480
cattatactg	cggttctgac	aaatcgttcg	aatccaaaca	gctgtcaaag	ataactacat	540
tgctgatgtt	ctcgtaccac	tattccacag	tcacgccgat	ttcctgcacg	tgattacggc	600
tttatctccc	gatgcggcag	ttgcatccaa	gcggatgagc	gcgtccggac	gatttgattc	660
atatctacag	tttgaggcag	aggattttga	tcacattggc	aaactctccc	atagtcggga	720
tctctcgcca	ctgtcgccat	cttcactcac	agccagccga	tagcggacgg	cagtcgtagg	780
cttgcttcgg	ccttatatgg	cgcataggta	aaagcgcgca	acatgacete	tctcccagat	840
cgatagtcaa	tggatccgtc	cgaaagcagc	cttcagtctg	cagtggaata	tcgttccacg	900
actcatcggc	aacgacctgc	tccggtggct	c			931

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 570 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...570
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:537

ccgtgcaaag	attaasaaat	caaataatac	caattcatca	gtagacagcg	gcaaacgact	60
ccgtgcaaay	Citycagoco	egggegaeac	adctdccacc	aaccgatacg	ggtgccggtg	120
tcctctatac	atctgaaacg	aaagteeage	agetgeeace	acceptant	ggtgccggtg	180
catctactcc	ggaaataaac	tgcgtttatc	ggeaggeaac	ccggccgccc	ccgtatcgat	240
aacgagaaaa	caaggcggct	atccacagcg	gcaggcacag	geaceaacaa	agacgaggca	300
teggetegat	aatccccttq	cgacggaatt	gatccgaaga	geettetgge	ggeageegee	-
agectaccat	ggatettteg	gtttccataa	cqtcataaaa	geetgeetge	aattagtata	360
ageacycca	cadccatcca	cagcgtcatc	gataatcttt	tttctcttat	cgaagagaaa	420
ageagggeea	cagecaetea	ctccttgacc	gatecaatea	gcacaaattg	ccaatcgcag	480
cttteggteg	egracada		acacatacca	aatcagagct	tgccgaatac	540
acagaaggca	ttctacccta	eeegrgegge	gcacacageg	~~~~~	tgccgaatac	570
cacggctgta	gagttcttga	gacgagaatg				

- (2) INFORMATION FOR SEQ ID NO:538
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 432 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...432
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:538

tttgactgtg gagcttctac gtcgtggcta tatcgggatc agctcggaat tgctttgggg 420 cgagaatttc ct 432

## (2) INFORMATION FOR SEQ ID NO:539

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1497 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1497
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:539

ggccgaatct tttgcccgat acgaatgctt gggttttcat cggtgccatg gaatctgtat 60 aagnagcate gegeettatg tggeggacaa acateatgte eggeegtagt gaaegtagae 120 agtacaggca ggtacgtggt ttccgtttga gcggtcatat gggtggagct aacgatctga 180 cgcggcttga tcgccttgcc atcggtggcg aaccggtggt taccacccaa agcgaccgaa 240 caggatetgg geattggata egetggette gaeetatgga tggaaageeg ttteaataea 300 ggcgacatga atcgtcccat ttcgctcttc gtggggggag cactacggca ttggtattgg 360 agactteggg gegaggagaa gattttttgg aaggtettgt eegeeteatg teegeetttt 420 ctactcattc gatgctgtcg acaggcggag ttcgacctca ttttggttgt ttctgcccgg 480 cacttggaga ceggttgeeg atgatetget actatectee tgetettaeg ateggagtag 540 ttgtcgcagg ctatgtgccc ccgaaggtat tgcggaacac atcttctcga aatacggcag 600 tcaggttatg cccccgaagc catcggtcgg atagccagat cgacatcaaa gccgaagagc 660 cgcttgtggc cgatctcgta catcgttcgg agggataccg ctacatatat atacgggaca 720 agacttacag ceggtgaagt agecaaceee teggaaaagg tatttgeegt taegggttge tacgagtage egaageeteg geaeggaaag tageggatat gggaagtett gtgtagagaa 780 840 gcagaaaggg cagctatcgg agggtaacga ttttaccttt gcgtggcaca gacagccgac 900 tecaceegta eeggeeatat egaaatagtg gagegggtee aggegateee gatetggtat 960 cggtgcgtgg cagacagttc tggaaaaggc cgatctgatt ctctatgccg gcagccttgt 1020 ccctegegae tgacegettg tgccaaagce ggtgccaegg teagaagtte ggetgegaga 1080 atctgcaaga acagttcgag atcatgtcgg acttttaccg ccgaggcaat tagtggtacg cctgcatacg ggcgatccct gcatctacgg tgctatcaag agcaaatggc actcttcgac 1140 1200 cactacggca tgcgctatca tatcagccgg gtatctcctc gtttcaagct gcagccgcag ctctgcgctc acagttacca ttcccgaacg tacacaaacc attatcctca cccgtggcga 1260 1320 aggegeacte ceatgeegga gaaagagaag etecatetge tggeacagte ecaageacea 1380 tgtgtatctt ccttaatgcc ggcatcgtgg acgatgtaca ggcgaactga tgatgcacta ctctcccgac acgcctgtag cggcctgcta cgactgacct ggccggatga aaaaatc 1440 1497

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 492 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...492
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:540

gagatgacgt	ttataaaagg	cctgacggct	aaagccaagc	agttcgcagg	tcgagcaata	60
gagacgacga	actotaacto	tgataaacgg	tgaactactg	gcttcggagt	tttttcgtat	120
ggacacccag	taggtttctt	ctgccaatct	acaagtagct	tgtaggcttg	atgccctagt	180
tattataget	taagacactc	ttgaggagag	gattttcttt	acgtagctgc	tctaactctt	240
attttaatta	aggggggggg	cactetagag	ggattgggac	actttcattg	ggacggatga	300
actttatett	caaatccaaa	tttactaage	caagagcgaa	tgaaccatga	cttagaccat	360
atttatata	aataactact	ttactatcta	acccgagagg	taatcctcaa	ggatgctaag	420
accedece	ttatttaaat	attaccata	atggatactg	gttgcatccc	gcccaactgt	480
		geegeeeuu	uegg	J . J	-	492
caacttttt	ay					

- (2) INFORMATION FOR SEQ ID NO:541
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 558 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...558
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:541

ggatcatcgt	ttgtatagaa	aaaccgctat	caaatcaata	ngtgtcctaa	tgtttgctta	60
gggggggggg	tttttagtat	gagagetgag	tegetecata	caagactttt	gggatttgag	120
gaggagagag	ctacctacaa	aaagagcgat	tttqttcttc	cggcggaggc	gaaaagggtt	180
cattgatcca	ttggcctttc	ttacgtcgag	ctgacgtgag	gttatcaatc	gcatagaaac	240
tcgacgaa	atcoccaaa	tctgaaacca	aaatccccca	aaaatggtgc	gagatctttt	300
cattataaa	cgagattttt	tcaactcccq	aaccaaaata	aaattttctc	agaccacgtt	360
tttcagaact	gaaatacacc	ggattttca	gtcacgtcaa	tcattcggaa	gcgaaaaagg	420
cactataeet	gaaagaatgo	gcagattgtc	aagttccgga	ccctgtggca	tcggatttgt	480
caytecydae	accasataas	accaaccaac	cattaacgga	ttataatcca	ctatgagtaa	540
aaggaccaat		accuacoudo				558
aayyaccaac	cggggcaa	•				

337 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 647 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...647 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:542 gtcccgataa tcttgcgccc gttgaactga ttggtgaata agctgtgccc cccttcgccc 60 atgagetggt egatecettt ggeeagttge ttggetttat eggateetga tttteaatgt 120 acttgaatag ctccggcgag aagcttgcaa accgcggaaa tgaagctctt cgccggctgt 180 cagogtatot coaatogaaa attgooggta togggoagao ogataatato acoggoatag 240 gettetecae egteteettg egetgegeea taaaageegt aggaetgetg aategaactg 300 tttgccgagg cggatatgct tgtagttcgt atttcgttcg aacgaccgga acaaatcttg 360 420 ccgtaaattc ctcctcgtgc gatccacttt cctctccact gcagccaccg gctggggaga 480 aggggcaate egacgaagea gtteageage teetgeacae egaagttgtt gagtgeegae 540 cgaaaaacac cggagcaagc tgtccggcca gatattcctc tttgtcgaag gctgataaac 600 accategate aattegatgt cegnaegeaa etteteaett gagtgte 647 (2) INFORMATION FOR SEQ ID NO:543 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 636 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...636 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:543

geggettgtt cagtagette tteageette attgeageag aategatete atageageeg 60 tateaactae aggagetgea tettetaeea aagtggeaaa teeatageeg tagagteage 120 agettettea gtettageet gagagtteaa gaagegaatg ataeagetge gattaeaget 180 geaaaageaa caaattette attteettt ggggttaaaa gtgtaattaa tgttetataa 240

cggcgaaata	tacagtttct	tttggtacca	ccaaaaaaaa	cgaccaaatg	ctgttgcatt	300
gagecetttt	atccqqaaqc	cttacgcatg	gctattcctt	ttaagacggg	ggcacccgat	360
cttgcgcaat	caagtataga	qqaaacqttt	gagctgtgtt	tgggtgtctt	ctcgaactct	. 420
teateatage	ggacaaaggc	cttattttct	cgtatgcacc	cacttgcccg	ttcagttcgg	480
				atccctttat		540
				gctctgtgcg		600
		tettegatee				636

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 880 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...880
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:544

60 agcatagtcg aagtggagtt gcgcagcaag ctcgaagagg tgcagggaga agtggaaccg ccatcctcat ggaggtagct acagggcagg taaaggcttc accaatctac agcgcacgcc 120 180 ctccggcgga tatatcgaat ccaagaatac gcagtagccg atatgtcaga acccggttct 240 acgttcaaga ccgtgtgatg atggtagcac tcgatgccgg cattgtgcat ccggaggaca 300 tcatcaaacg ggcaatggtc tcttcttccg taggcaagcg tactgtaaga gacctaatgc acacaaagga gggtatggcc cccttacggc agctcagacg attggtactc aagcaacgta 360 420 ggcgtagcca aaatcattct caaaggcttt gccacgatcc cgacaaatac gtggaggcgg 480 tcaggcgaac cggtatcacg gcaagttccg tctggaaata cccggagaag ctccggccgt 540 agtgcgcaag gtgccgacaa teetgacege tggtatggca egaceettge atggatgtet toggatacga aacccaaato cogoogatoo atacattggo tttotacatg cogttgooaa 600 cggtggtaga atgatgcgtc cctacttcgt aacgaaatga tggatagagg ggaggtcgta 660 caggagcacc ggccggtagt attacggatt ccatctgcaa gcactctacg cttatcgcca 720 780 tacaggatat gctctgaacg tagtggccaa agggaccggc tcgccggtca aaagctctac 840 ggtaacatca geggeattga eeggtaeage geagatetea eagggeaaaa gegttategt 880 gcaggtggca ccatgcactt ggtattcttt ctgtggttat

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 604 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...604
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:545

gcagaaaggt	tggcttatcg	gtgggcagca	aaacqtatca	cottotatas	ctcggagagc	
aattcattcg	agatcaagat	gangetagen	t-	Coccocgica	ctcggagagc	60
CCaacagaag	agataaa	gacgetegaa	ccgattcaga	actgcgcatc	aacctcacag	120
acagaac	cyacaccccya	caaacqcqac	ccaatacatc	tatoccooca	+ ~ ~ ~ ~ ~ .	180
ocacygayga	aacticigat	gacgaccatc	qqactqaaaq	acatattcea	anattast	
ggagcacggg	ctatgcctcg	caageettea	atcacttcat	ccacaatcgg	Cagciegiee	240
agggggtatt	ataactaset	atastassas	accageteet	ccacaatcgg	gagaaatcgc	300
200224	acyge ceaat	accatggage	cacttatccc	tctccggatt	catggaagga	360
jumageeeg	geeggeeage	eggtttette	tgaaaccagt	accattatat	annah	420
Jacgocca	ccccggcccc	cicagtactt	nanantoata	atasataaas		
tgtccggcat	cccctcataa	ccttccettc	ttasses	gccagcggga	aaaatcggcc	480
ttnancasas	ananat		Licecaactg	ggaatgtcaa	gctacacggc	540
jugodada	ccyaactget	caagaaatac	tttccggaat	ggtgcgtatc	aaccatactt	600
accg						
						604

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 502 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...502
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:546

caacccattt agccgaacac cttgacggtg taaagatgtc tgcggatgcc gtacatagtg	cttctgcaaa	aggaacttct gatcttttac attgctgtat gttagatgcc atgccctgtg tactgcacct	cttttgttca ttttcacagc ctcgcgaaga gtggggctac ggactgaatg	aaggttegee etgaceggee eggateattt egattateae etaattgtgg	ccatgatatt tgcctgtact catacaacgt	60 120 180 240 300 360 420 480 502
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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 626 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...626
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:547

tgaattcttg	taagogtata	aaacctaatt	ctccaacctg	acataagcct	caggeegaae	60
ttageceage	gatggaaacc	ttcccqcaaa	qaaaqagcag	cgtattgtgg	tactcttcca	120
tacqaqtqqt	atcattcaac	agcgtgacat	ctctccqqca	tcattcagtc	gtttgataaa	180
cadattagga	taaatcaatt	gtccaaagga	ttcttgacct	tgaagcgacg	gcgacttttg	240
gtatattgaa	agtgtgggaa	atactaccca	cgggcacgaa	taccatcgta	togacaaatg	300
aggaggeteg	aattcattac	catcataata	ctcaatctat	ccccacgata	gaaaccgagg	360
ttatagagat	aaatcaaaca	agccgttcct	tacaaaacaa	attgaacata	ttattgccgg	420
cegeagegae	gggccagacg	acastacasa	ttcattcatt	ccattggcaa	aattacccgg	480
gaaacttcac	agtgatgatt	cataateeee	ccattctccq	tcatcagata	gtaattgttc	540
acggateacg	ateggetteg	taacaataaa	aaccatact	gccgaagaac	ggtaggagat	600
			uucggcugee	9009449444	9555	626
ggetttegte	ttgttggagt	cycana				

- (2) INFORMATION FOR SEQ ID NO:548
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 433 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...433
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:548

gaagaatggt acgagcagat cattttgctg ttgcttgcat ccgtttcgac	gtaaagagac tgtgacgatc tgcaaactct cgcagcggac agccaaaggc	gggtggcaac caaacaggca ctatagcgtt taagcacgaa tgcatcagca	gtcatcgcga gaaccgtctt gcgcagcaga tcttgctctt ggtatgcatc	ctgaccattg taggctgtcc tgttgccgag ttgatcacca tgcacatctt gctgcataag tcggcaaaan	attatectet acagecagat ectgetetat cattteacae eggtaceaaa	60 120 180 240 300 360 420
gtctacggaa aagccgactt	gatagggtag	gatcaggtag	cttgaccact	tcggcaaaan	tcgtgtgata	420 433

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1237 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:549

cageggggat getgatggge aacttaceaa ttettgaeat aatteegtae teetttatea 60 ataaacgtaa cacaatactt ctcccccaac tttcaactac gagcttcttt atcagtcatc 120 actectegtg gggtagaaac aatagcatac caaggeegtt caataegegg ggcatateac 180 gataacccac atacttcgaa ggccgggacg agacacacgt ttcaactttc tggatggcat 240 ttacttatgt gccaaatcat actttaaggc aacttttatt atgccttgag agtcttctcc 300 togaacttat agttcaggat ataccetttg tegaaaagga tettgtgate tettettaa 360 tatttgacgc cggcacactt accacacgat ggcagccata attgcattac gcaaccgcgt 420 caaataatct gcaataggat cgtcattttg aattacaatt aaattgatcc ggaaagccgg 480 acaatattta aactettace aactegettt ttttacgeeg gggataagae eggeagaage 540 atttcacgaa attgaatacg ggaaatacca aattggcgca tatagccctt ggacgcccag 600 tcatcgagca acgattatgc aaacgaacag gagaagcttc ttagggagca actgcaaggc 660 ttcataattt cottcagcot tgagtgeget ctctttgcag catatttcgc cacaagcttg 720 gcacgcttca cctcggggct ttcattgatt ctttagccat atcaattttg ttttttagcg 780 ttctgaacgg taaaccgaat tctttcagaa gggcataacc ttcttcatcg gatgcgccga 840 agtcacaaag gtaatattca ttccgagaat cttcgtaatc gctcgatatt tatctcgggg 900 aaaatgattt gttcattgat tcccaacgta tgttacctct tccatcaagc ttgctttcga 960 taccettaaa gtegeggatt gaggeaaage gatgegeace agaegtteea agaacteata 1020 catttgctcc gacgcagagt aaccataaca ccgattggca tcttctttct caacttaagt 1080 ttgagatgtc tttcttaaga tacccgtcgg tacagctttt ctgtccgtaa tagcccgtca 1140 attogettae tgeaacateg ataatettet gteacegtag ceataceaag acettggttg 1200 atcacgattt tetteaacac aggaetgeat caegett 1237

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 665 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...665
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:550

taaatctttc	atcaagtaac	catagattat	gatcctcata	tccgatttcc	tatcatcctt	60
aatcatagga	aatattaggt	tatgcatttc	actttcttat	gtgattttcc	accatctatt	120
cttttacgca	aatcatcaaa	caattetta	ttctacgtct	ctggcaaaca	taatgagcca	180
aatcattctt	agctgttctg	ttacattttt	caagatttta	tttgcttcat	cttctagtgc	240
gctatgcaac	tttcatctcc	cgatgagtat	ttatcttgca	attcctttaa	tgcttccttg	300
cattttgctc	tttgtcaaac	tttattttt	ggaagcgcat	ttcaaatcaa	attctgaaac	360
tcctattgga	atagattcca	tatctacqtc	tttaacaaag	tcttattcca	aggtgctgta	420
qtatatacat	aatgttcgac	ttttgcttct	tatcattata	teggttttct	atgtcttcgg	480
aaaaatacgt	ttaatggatt	aatgaagttg	ttttcattat	tggttctcag	ataaatcaga	540
taaaatgtca	tettetttt	ccaaaaatgg	aaacccatct	tetttetgtg	gtacnatttt	600
catctagata	tttacccttq	gaacatacco	cttttaacat	ggtagtcctt	ctggagttcc	660
atggt		J / J				665
acgge						

- (2) INFORMATION FOR SEQ ID NO:551
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 558 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION 1...558
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:551

gcggacattt t gaaaatgaac g gagaaggctg a atgtccccgg a agggttcaaa g gagaacaaac t acttcgatac a acngtagtgg t atgatcgacc g	gtatcgatca attatgccaa attccgaagg gcagaggaga tcaatgtact cactgacgac tagacaagag	agaatacgga cgaagtgaaa ggatggtacc tcaaccgcgt gggagagcct tttgaattcg cttcgtgttc	tgccgtcatg aagctctgcg gatgggtatt agtcggtcgt atgcctaacg tatcgacctg cttattatac	ccattgctac tacctatcgc gatcaagaaa gaactctatc aggattgcag gctcttcagc cgatccaacc	ggtagcaatc caacgtgcca atgtacggta gntaatagca aaggagtacg cccgtggtgg cacagaggag	60 120 180 240 300 360 420 480 540
atgatcgacc g		tctatgagat	ccagctacgg	acatteggtg	gaageegaca	558

- (2) INFORMATION FOR SEQ ID NO:552
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 521 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...521
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:552

gategetgac cttgagagag cgtccttttg cggcagcatg agaaaaagcc actatcaaag		tgaatccaac gaatgataag ttatccgcca aaaagagaaa tgcatcgaag	ctctaacage tttteggtgt catttgtcag agtcgtatcc aagtttegge	gccatgggca agttcttcgc tccttctctt ccggtagaga tccttcgcat ttttcgccg	tgaccgattt tcggacataa	60 120 180 240 300 360 420 480 521
----------------------------------------------------------------------------------	--	--------------------------------------------------------------------	--------------------------------------------------------------------	---------------------------------------------------------------------------------	--------------------------	------------------------------------------------------------

- (2) INFORMATION FOR SEQ ID NO:553
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 446 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...4\overline{4}6$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:553

tacaaaagto ggttccatat atttgttato gactatcaac nggaaaggct	ccaacctctt gcgcctcgac ggtcgattta aaagaaatct	ttattcaaat tatttttta gcngtcacca catataatcc aatcttacgt	gtctccttaa gttgtgtttc atgctcatga	tatttggctg ttccaagtca gccccttgat attgcacaat	ttagatggca acactgataa tccaactttt actgtcggcg ctgatgaaaa ttacgcagaa cttctggtta	60 120 180 240 300 360 420 446
--------------------------------------------------------------------	---------------------------------------------	-------------------------------------------------------------------	----------------------------------------	------------------------------------------------------	------------------------------------------------------------------------------	-----------------------------------------------------

- (2) INFORMATION FOR SEQ ID NO:554
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 667 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...667
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:554

aggatactcc	ctttgattcc	cccagggctt	gatogoagoa	agggtattag	tcgtagcggc	60
ggcatgetee	angettage	atcodoctot	ttagctcatt	ggcagagca	cgtgatttgt	120
gegatatage	testes	accegeeeee	gaggetegaa	aagcattgca	ccgattctct	180
aatctcgggg	tegtiggite	gaateegeaa	ttttactatt	actaatettt	cegattetet	240
cagcttggta	tgagaatcgg	tgeagtettt	tittactgtt	octation to	tcaacacctt	300
ggttcgttcc	ggatttctaa	agggctgaaa	ggaaaatcgc	agetteate	gcctcgtttg	360
ttgcggataa	tccttatttt	tgtatccatt	taagggataa	taagttcatg	tcaaggaaaa	420
accataccca	ctatctgttg	ctctggatga	cactctcctt	ctgatcgtat	gtttgcctct	
ggagggccaa	cggaatcgcg	ctttaccgtg	gttatcgatg	cccggacacg	gaggacatga	480
ttcgggggca	toggtaatgg	tttacgagag	aaagacatca	atttggcccg	tggctttgct	540
ataggacgac	tgatcaagag	caagcattcc	ggatgtgaaa	gtgcttatcc	cgtgaagaag	600
gatttcttcg	ttaccctgat	gggaccgtgc	cqaatatcca	ataaaaacaa	tgcccgacct	660
ttttatc		333	-			667
LLLLace						

- (2) INFORMATION FOR SEQ ID NO:555
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 430 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...430
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:555

caggacgcaa	tcctcggaaa	atggctgcaa	tgattttgtg	teceteatet	gcgcaaagaa	120
catggctaca	gccagaatqa	tcaggaagag	ggaagaatag	tccccaagge	gcaaacggct	180
gctccggcat	atectegagg	custages	772274444	tetetagge	gcaaacggct	
Caaacaaast	taaaaaaa	cyacayccia	cyaayacgga	tatattgacg	gcaaatactc	. 240
cgggcgggat	Lycycaaegg	caaaaagatc	cagaaaatcc	tcctccgata	gccatggtgg	300
LLatecacta	tateggeett	gatcagtggc	aacatggcat	aacttcaccc	gaaggtgaat	360
cccgccgata	ccggaaaaag	gtgagaaaga	aggatagata	tggatttcac	ФФСананана	420
gaagaccact				33	,,,	
						430

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 568 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...568
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:556

gcccgaaata cggaaaatca aacaaaatgt ttcactaaca aaaaagataa cgaacatgaa 60 aagattatta ctctctgctg ctatcctaag tagtatggtt tgtttaatgt caatgcacaa 120 gagttgaaaa cctctgctga catgaaagtt cttttaagaa gaatgtggta ttggaggtat 180 ttactgccga atggtgggtt actgtccagg tggaaaagag cgcattgcaa aagcaattga 240 aatgtggatg atgaatataa ggagcgtgtt tttcagacat ttgttcatta taatatggga 300 tctcaaaaaa atggcctcgt gttggccaac ttttcattgc attgatcaaa cattgggcat 360 tccgggtttt ccgacttttt tcagtttgcc gttggagaaa aaaggtgaaa atctttcaat 420 aggtgctcca atagcaatta aaataagatt atgaaaggtt ttggtgatgg tacagcccct 480 gcagaggtaa cetttaaatt gacncaaagg tgcaacaccg gaagatgtat tgtaccagca 540 catttacctg gtaaagtcga tgcctgac 568

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 647 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...647
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:557

ggaaaatttc	caaggtcgtt	ctcgttttac	tttaattgtc	cataatgtat	ggtaattagc	60
atottotaat	gagcaccgta	cgcctacgct	ggtctcctca	tegtgeagga	gtgcatcgta	120
cacctacaat	cataaatatt	tegtaceget	tttcaacact	tcttcgtatt	cctcggcata	180
atcttcaatc	togtacaaaa	ggtattgcct	gagagcgtag	ggagaaaagg	gatggtttgc	240
actecaace	atgccgtact	ccgacaagat	ttattcagat	ggtttagaaa	ggtgagtgac	300
gytyaaaaag	acgoogtace	ccgacaagac	cattastaca	gcaaaatttt	gaaggtcagt	360
gggtaagaag	agtoggttag	ctgggcaacc	atasatagag	aacacttctt	tccaatttat	420
togggaacaa	tttetgtgag	attgagtgaa	gccaacaggg	gaataagat	tataataaat	480
tggcgcgcag	gcgttcgtaa	tategegace	gttcaggtag	gedateaget	tctcatgcgt	540
attgtagtta	cccagagttc	ttggaaaact	gacgeteegt	cttcgcaaat	gacctccttt	
ccaagccgga	caatcgtagc	agccaaagca	ccggcgaaca	gacaatcctc	gtactcatcc	600
tgttttgcca	gcccgaagcc	agtaccatga	ccggctttgc	ttggcga		647

- (2) INFORMATION FOR SEQ ID NO:558
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 367 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc_feature
      - (B) LOCATION 1...367
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:558

tegteagtge etgetetttg gtgtgettge agetgtenga	caaatgtttg tgatgctcgg agtcctctcg tagatgacaa	gagetgagge agaegagage acctegtegg tttetteetg	acagectget agaaagtege caatcatate atgaegeece	ggcaaatagt gtcnagaaag ccgttttgca	tgaccgtatg ctccgacctg agaaagagag gggcttgcgg	60 120 180 240 300 360
atgagatcca tgctgtg	acgttgccgt	cagaaaatct	ttctccatgc	gttcggacgg	aacggttcgt	360 367

- (2) INFORMATION FOR SEQ ID NO:559
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 472 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...4\overline{7}2$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:559

agccaacatg	ctccgactgg	atttaataas				
	occegacing	accigetega	agggetgete	acgaagetgt	gcgcatacgg	60
gcagcgatca	gggattgage	ctgcaagtaa	ccatattaca	~~~~ <del>~</del>	J - J - H - H - G - G - G	00
gaaggteeta	tanaan		eegecctacg	geegattaca	catattgtag	120
55500009	ccuggaaccg	aaaqaaaatq	atcgaggagg	+ annunger	~ a + + +	100
tcttagaaat	CCCGacttat	atcccaaaa	~~~~	1	acaagagteg	180
GBGGGGGG	+-++	geececaace	ggegaactee	tccttccata	acaagagtcg	240
	ceceggeege	acataaataa	cttqtatctt	tatacasata	+	
Caaatactat	tcccctttta	+~~~		egegedacta	ccgatcttat	300
	cocccccca	cygaactaaa	aaagactaca	cqttcqaaaq	ccgatcttat	360
cggagaacgc	gagatacccg	gccatattct	attagagtag			300
aacttoooo	*	3-04-04-06-0	attggcgtac	agaegetgeg	tggtatagaa	420
adceceeea	ccagcaattt	tatctgaacg	attacccct	atttatcaat	aa	470
				Joodaccaac	99	472

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 777 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...7\overline{7}$ 7
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:560

tttccgagcg	attacaasaa	a+ ~ a				
	geegeggage	argaaaaagc	ataattgcgg	atcqaaaaaq	atggttcgag	60
aaaaaaataa	aactcgagcc	aaaagcaaaa	aaatctcgg	atannantt.	h	
togagttttt	gagatttag	gatarret	addeecegge	graaayartt	tccttgtggt	120
5 5	Jagaccccag	gereggeatt	Clecatett	CCCCCCCCC		180
atatetacte	ccgaataaca	atctctccgg	aatcatttct	ataggaggag	atggatcagc	
ttgtgcctct	cdatcadtct	attaa===		acaggaggeg	arggateage	240
+~~~	ogaccagece	accaeggggt	atgeeggtet	tegatteggg	ctgtcggaaa	300
22 - 22-00	9909909000	Cyclicated	Ctacaggggt	atasssstt		
ggattaacta	togaattatt	tastsaattt		gegadadatt	acagtcggta	360
++++++	- 55440040	cyacaccccc	getttgtggt	ttagcatatc	acagtoggta	420
	Janagaagte	aytacacaac	acqaaatcac	ttasssan	+ - +	
gaaatcaaat	cagtetgatg	taccacasas	+	·	cacgaagaag	480
222272±222		caccycyaca	rgrggeagte	gtcaggcaag	taccaaccag	540
J	o oggaacgca	Layereegt	tattataaa	ataggttgt	+	
gaaacgaacq	gaggtgcatt	Cdadcadata	notatat-		egegegageg	600
acagtgaga_		cgagcaggtg	aateteegta	rggggagaac	CCCaacaaaq	660
	o o o o o o o o o o o o o o o o o o o	accyclaacg	aagcgggtat	tcacacacac	a + +	
gcggactcaa	cggactcgta	tattccccat	200000		acgeeggaee	720
_	55 00 g 0 a	tgttccccgt	accyyctgat	grgcgccggc	tgatgta	777

# (2) INFORMATION FOR SEQ ID NO:561

(i) SEQUENCE CHARACTERISTICS:

348 (A) LENGTH: 685 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...685 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:561 gaaaacttcg actctattgg atccccgcga atttgggaat gaatacagtc agccataacg 60 tegggeatgg teatgaaaag categegeag teeggtatgg eegatacaee geeggeeaag 120 gccacttgtt tgatgctatg atctttgccg cttggcgaag tttcttcatc aagatgtcta 180 tgaccgtgtg ctgaaggatg cgcacagatc ggccttgttc ttttctatga agtcgggatc 240 ttcggcaggt tggtcgcgca gagtatagag gaatgatgtc ttgagtccgc tgaactatag 300 tegtaacegg acacatgagg aegggcaaag eggaaageat egggttgeee teggaageea 360 acttattgac gatggggcct ccgggataac ccaccccatc accttggcac atttgtcgaa 420 agecteteeg getgeategt categtetgt cetattacet ceatategta aggggagega 480 540 accagaataa ctgagagttg ccccctgaaa ccaacaagca caggaatggg aaagagggag 600 ctgtgactcc tacccggctc acgaaggaag ttggccagga catgggcaga aagatgaatg acttccagca tcggaatgcc caatgaaagg agacaatcct ttggcaaaag ctggtgccta 660 685 caanggageg ateceageaa aaceg (2) INFORMATION FOR SEQ ID NO:562 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 765 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION 1...765 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:562 ggetttttte geaatttttg egatggettg tgeatgeeag ggagggaege eggeaagteg 60

ttcaccaact ctacaggate teegggegaa atgatgetgt catggaegae caatatetgg

gategeetgt eggegaagee atetaeggge aatgaeegag gtggeteegg etetgaacea

anacgageeg ateatgetgt ttegegegta tegganangg attttaeggg etteeteege

tatatogoaa tgtgotgoag atogacatoa accoogatat attoaccaag actttotoaa

120

180

240

300

atacggctat gaccagtggg ctaacggtca gctcgtcgtg ctgtcaacag tcctgcgaca 360 gattcactga cggcctacgt cgaatccaac aatcggccat acagaacctc tttatccgcc 420 acgagetttt eetettegge egetttggea gaaagaetge agtgeggatg eegaceageg . 480 cgtacagcgt tgttcggata ccatatcaat gtgccggccg atatactcag ccacaaggag 540 gcaaagactt cctgtggatg tccaacaatc agatgcgccg gcgcaaggtt ttttggtata 600 tactttcccc tatcgcggag catcggatct gggactcatc gtatggtgga ggtgcgtgac 660 teegtgetea aageeaatat agaaggtegg aegeagggte ttateeegte aegaageegt 720 atgctactga agcatgttac gtctacccgg gcgaccaaaa gcagg 765

## (2) INFORMATION FOR SEQ ID NO:563

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1813 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1813
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:563

ccatcgatct gtctttggcc ggtaaggcgt cctctcattg gccgacctga gcgttctcga 60 totgatagec aataacgaat ggaagegtee tatetattgg etattaegte teegageaat 120 tettteteca acetgeegga ctaettggte agaceggtat ggeeaateag tttgtgeett 180 ttaaggegeg eegegtggeg ataacatega tgtggaaaag acctatacea atgtgatgae 240 caagtccgct tcggaggggc caacaatccc aaggtgtact tcgatgcaga tattgcaatt 300 ccaccaatac ctategegta getgtgttt eteegttgge aaagetetge tegaaagagg 360 cgataccgtt cgtgcccgta aggtgctcac caatgcctcc aagagatcag tcctgaagcc 420 gtgccctatg attatcgctc gtggtattgg cacaaaccct gtacgatgca gatatggtgg 480 ccgacgcaga cggatagtca aggccgtggc aggctcttcg atgcgtacgc ttaactggtc 540 ttccgcctgt cggaatccaa attcatgcaa atgctttccg aaggagagtc gacagggaga 600 tgaatacggt tgctacggct cttcggctga gtactgctat aatagcaaag tgttggatga 660 atatetgece gtgtteeaga actatttaag atgetetaca etgatgagea gggtaatage 720 aaaccgcaat aaatgagctc agactcgtag aacgacttat ctgccgtgtg cccatgtggt 780 accggetttg tteeceggtg ecaegtggeg catteetgee aaagaaggaa aaacatetat 840 ctgactttcg atgacggtcc cataccggag ataacaccct ggtattggat acgctcgatg 900 aacteggggt gaaggeeacg ttettetgtg tgeggataat gtgegteget atecegaact 960 ttttgcccga gaatacagcg cgtgggtcat caggtcggca atcacacttt ccaccatctg 1020 caagggetga agteegtaca egtacetate tgaaagatgt ggaagagget gacegactat 1080 caattetege ttetttegae egeegeatgg ceatettege tteatgegae eeteetgett 1140 agcaatcact acgacattat tatgtgggat gngatccgcg cgattataat gctcgccttt 1200 caccegatae egtetttggt teggtgtteg etatgegege aaeggeteea ttattaeett 1260 ccacgactee etcaagegge teccaatatg cageaggeea tgeetegege tgtgegetgg 1320 ctatggatga aggctatacc ttcaaatgtc tgggcgaccc ggccgactaa gcgtttacct 1380 gttttttetg teegatgatt gteettaegg aagaeggate teeactatee tttegeetea 1440 ttacggcgaa tactaccact ccatacacgg gcgtgtcgtg agagcgaaca tgtattcgtt 1500 catacgggac tgttgcacct ttggaatctt tcgatccttc cggtactttg tatctctttg 1560 aagtoggato ggaacggoto toaatgogot actgaototo ogogaacaao gatgtogggt 1620 ctctccatcc attactctgc cattgagaaa tttcctctcg aaagggtgta tatgagcatc 1680 ttcgcttttc tgtgggaatg gctgatgaag acaaatcctg caaagtctcc accatgcacc 1740

gtggggaatg gattgtgaaa tatgcccggc ttcacgttgc acaagatagc atccgatctg 1800 accgatttac att

- (2) INFORMATION FOR SEQ ID NO:564
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 466 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...466
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:564

cgatggatat	gaccgagttt	ctggcacagg	attacgatga	tattcgtatc	cggtcaatgc	60
attacatttc	tetatettea	acgaatcgat	gaaagtggag	tcgtggtact	gcctgtattc	120
gagggtacc	gtctgcctgt	ggatcctgca	atccttggaa	tatcttctcc	ctttcgccca	180
ttgctcaggg	gatgaaatcg	tctggaaaga	agaagccggc	aaaccggcct	tcaaggttgc	240
caatacgagt	acqqtqcqcq	atggagcact	acgeteteeg	gtatcgactt	cgcttggctg	300
cattgcatac	atggaacaaa	gatgcccgtc	atcgaagtac	aggcattgtg	ccgacggaaa	360
tcatcatage	cctccctatt	aatcgtatgg	gatggtcggc	ggcgacctct	teegtaceee	420
		ggagagettg				466
googgaoago	- 9 9	33-3-53	_	-		

- (2) INFORMATION FOR SEQ ID NO:565
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 631 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...631
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:565

gaggatecee ageggaeatt etetetgeet aacaggtgga ggatgteate agggaattga ttaaggagat agacaagete ggagtggatt eggtttggte gtaattatea tttegttett

categgagee gttate	cacta tecagettet	ctgaatatga	cctctccgct	cattccgcgc	180
tttacgatag gttatt	caca cgtgagatca	ttctgttgga	gttttcttcc	acggttatgg	240
ggtetattet ggeegg					300
gactgagcag atcgat	gcta tggaggtgat	gggtgtgaac	tcgccaatta	tctgatcctg	³ 360
cctaaaatca tcggat	tcat gctgttcgtt	ccgttctgag	tataatcagc	atgtccacgg	420
gtattgtcgg tggtta	itctg gctgttcgtt	ggtgccgaat	ttgcctcgga	gcgactttga	480
gtacggtttg agcttt	tett tteeecttat	aatgtgtttt	actccattat	caagtcggtg	540
cctatgcttt catcat	atcg agcgtggccg	gttactacgg	ctatacggga	aaggtggggc	600
atttgcaggt ggggaa	agca gtaccaacgc	t			631

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 929 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...929
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:566

```
ggcatgtgcc ttggtggatg ctttctactt gcaactggaa aggaagtatg cgagctatac
                                                                        60
aaacgaagcg tagcaaaaat ggaggaagac cgtccgcaaa ggaaatctac gatatggatg
                                                                       120
ttogtaagat caagatgaac tattggottg cotottotoo aagagtottt ggatgootta
                                                                       180
tgggatcata ctggcttttt gttgatttgg cttttcctct catgcttgca tccttgcgga
                                                                       240
ctgccactat ctgctgcaaa taagccggaa gtggaatgaa gaagatcgtg atagcataga
                                                                       300
ctccttcaag ggttgtctct cctctgccga ggcaggagaa gcagcggtat gggaggtggg
                                                                       360
ctgttggctt cacaccccga gcgattatcc ctggggtatt ttttgtttat agggtgttgc
                                                                       420
atttactatt ggaaaataca tataatctca ccctttatgg gataatcaca ttgcctttat
                                                                       480
tgacttgtaa agattgatta tgaatcaaat gtctttatta tatttgcact gagtaaaaaa
                                                                       540
ctcactctac tgagtaaaat gtgcggatat gtataaaaga gcagagtaca tgtgattaca
                                                                       600
gatcgtctta aagatcggag gagattcatt caagtcgaat gggggctcgt caaatcggaa
                                                                       660
aatcaacggt tgtcaagcag gtgctgagga cttggatgca ccctatcagt tcttctcagc
                                                                       720
cgataatgtt ccgacgtgaa cggtgcttgg atttccgatt gttgggctgc tgtccgtagc
                                                                       780
ctgaggaggc caaggagtgg gagagcatta ttcttgtgat cgacgagata caaagattgc
                                                                       840
taattggagt gaagtcgtga aaaaagagtg ggacgatgat acttccatga ccgtaatatc
                                                                       900
aangtgttgc tgtttgggca ntagtcgng
                                                                       929
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 676 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...676
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:567

```
gggaatgggt cttccattga ctatgatttg atgaaattaa aatccggcca ccaatcggta
                                                                       60
                                                                      120
atgeegaaaa aateagetee acaaaggtaa gattateage aaaegaaaaa gatgetttge
                                                                      180
attcagagac cattgttttt getetgaget ateggeaaat gtaeteatee tgeaaaaaag
aagagggcga cccaagatat ttggatcgcc ctctgttctt tatgctaact tcattcagag
                                                                      240
ggctgcggct cctcctgaaa aaagtgttgt cagatcatat aactttattt tttgcatcca
                                                                      300
ggctcgcact gatgaaattg ccctgtgcat cgaacagcaa atctactcct tgttgttgta
                                                                      360
cacgatttcc gccttgtatg tgccgttgga cttctttcga tgtccttgat aaatgcaccg
                                                                      420
                                                                      480
gggtagttcc ggttgacgta atgatgatct tagccttgat gtgagcagga atgttgtcgt
                                                                      540
catcatcctg tcgtctacgt ttccgctgat gaggttgccc tgtgcatcga acagcaagtg
                                                                      600
tactccctat ggtgtagtaa attctacgtc ataagtacca tggagttagc tcgatacttg
tgaatgacag cttcccggta attctgatga catagctatg atcagagcct gatgttggcc
                                                                      660
                                                                      676
cgaatgtgtt tcgatg
```

- (2) INFORMATION FOR SEQ ID NO:568
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 493 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...493
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:568

ggctggagaa	taacaagaaa	taaaaagacg	atgaatcaat	tgaccttcac	agaaaaacga	60
				ceggtetect		120
				ttcgggcgga		180
				atttatgagt		240
				gtgttggccg		300
caccgtcttt	ttgaagaaag	tctgaaaagt	cgcgagggtg	cccctcgttc	gttttttatg	360
				gtaatggctt		420
				agtggaccag		480
ctgggatact	acg					493

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 359 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...3\overline{59}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:569

cctgcccgtg acagtggata agtccatgat cggtgtaccg ggttgccacg tggcatactc 60 attcttcgca agacggaaga aaagaatggc cgtacctaat gatcgacacc aacgactctg 120 aaaatgactg tatagcccgt caaggacaaa ctcttttcct gcaagattct aatagaaaag 180 tacattagta tatctcgaat atagactccg aattattctt accccgatct gtgcagacag 240 tgtcaccctc aaaagggcga ctgtctgcat agtaatttga tacgagacac ctcttgccca 300 gatcgcaagt canggggctc gaatacaatt tccgatgatc acagaaaaaa gaatggact 359

- (2) INFORMATION FOR SEQ ID NO:570
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 562 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...562
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:570

gcaacttcgc	ccctatataa	~~~~ <del>~~</del>				
	ccccgcacga	gaageetata	ccgaggggca	ageggeeggg	cgaaaagaat	60
agtagccggc	aagccgatag	tettegaaat	gatagtag	2222	- Januaguuc	00
atagggatag	taggatt		gatageeteg	ceggtegaat	cgaaaagaat	120
333	daggettegg	Cyclycgaga	gcattccagc	cgatgcattt	ataastass	100
cgtgagtagg	aagcacgccc	tacastataa	antamtt	- 5	gegeatgeea	180
attogggggg		egedatgtgt	catagitacg	gacactgatg	cgaccacccg	240
22-2-5	~gcgaggagt	ayrtatiqcc	gttgtacgga	agatagtogo		
ccataggeeg	80000000	22224		agacageege	cegeatateg	300
222	- you gauacy	aacataqqçc	gaatcgcgca	actatogoto		360
gareggeeee	ccttttttct	ttcatttaca	Caaaatotoo	atatati		
agacaggacg	atatasta	J J	ouddate tee	cigialigee	tttcggtggg	420
	- occaucing	aayeteyaaa	ggagtattga	geatetgege	ataasass	480
aagtgcacag	tcccaaaaaa	Caaaaaaaa	~~~~	J	ceegacagac	400
- 3		uuuugaaya	gagcgaccgg	aaggcggctg	tatcttacat	540

60 120

# (2) INFORMATION FOR SEQ ID NO:571

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 511 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...511
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:571

gggaaaggcc agccccaaac tectegatgg tateatggte atgtactaeg caacgccaet 60 cetetgacae aggtageate cateaataeg eeegatgeaa gaceategtt gteaceeegt 120 gggagcgttc cctgatcaag gatatagaaa ggctatcatg gactctccgc tcggcattac 180 gcccgagaac aacggtagct gatccgtctg ggccttcctc ctctgacaga agaacgccgt 240 cgccattggt gaagcagacc aaaggagatg ccnaggacgc caaggtgagt gtgccaatgc 300 ccgtcgcgat gccatcgatg cgatcaagaa aagcgtnaag accatggtac tcctgaggac 360 gtagccaaag atgcagaggc agagatgcaa gaggttcacg atcgttatat caagaagatc 420 gaacgaaact ctttgcccga aaggaaaagg aaatcatgac ccgtgtaagc gtgaaaaatc 480 511 tatccactca cgattgaaag ccagagtttt t

- (2) INFORMATION FOR SEQ ID NO:572
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 955 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...955
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:572

gagtaccgtt tcgctggtgg catgtaccag acttctacca tatcgccgtt ttgaggaact ggacgccgtc gatgctcgca cccggtatgg tgatctgccg aacgtttcgg ggtgcatgaa

gttgtatccc	atctcgtcc	gatagagtac	tgataggggc	gtcgttctat	tctgacctct	180
			cgaggatacg			240
			gggcttgacg			, 300
			ccgttgcgaa			360
			agggtagggg			420
			tgcggaggca			480
			gtgtacattc			540
			ggttcctttc			600
			gcagtatgtg			660
			gatttgtttt			720
			tggtttgatg			780
			gaaaaagcaa			840
					gtcagggact	900
			tcgacttcct			955

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 433 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...433
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:573

ggtatatgga	gcgtcgggga	agcgggataa	agaaaatctt	tgaagcaaca	agaatcttta	60
tggctatacg	gaagaaaaaa	agccgttttt	ccttgtgata	aacagaatga	cttcttcctg	120
acgattccga	acgttaatta	tcgttctagt	ctgttaccac	acatgacacc	atacatgaca	180
ccatacatga	caccatcatg	acaccataca	tgataaaatc	gccttgntac	tttccttctg	240
tcaaagcctc	gcagcagaga	agagatgatg	gagtttgtgg	gtttaagaaa	ccgcatcatt	300
ttcagaagaa	atacctccgt	cctttattag	aacaggaaaa	gatgaaatga	ccattcctga	360
aaagccccaa	agtaagaacc	anaagtatcg	aagaaggagg	tagtcaaata	acatatccat	420
tctctaatat	aag					433

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 567 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...5\overline{67}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:574

- (2) INFORMATION FOR SEQ ID NO:575
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1008 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION  $1...1\overline{0}08$
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:575

acgccaaacc ggacttcage gacgaagacg gtacacgggt agcagagctg aggacaaatt cgccgaaatg gaaggctgga atgccgagag cgatgcagca tgttgctgag acgacgcaca tatgctgta aggacttgag cggaaagcaa aggaccacac cgacccgacc	60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1008
ctggacaatt cgggctattt cattacggat beganning cgtatgctgt cagcggagag ccaaggatac gaacgaaatt tttctcaaag gttcctcggc cgtatgctgt cagcggagag gagattctca aaaggcatcc tcctctccga gggagaagat ccgtgatg	1008

# (2) INFORMATION FOR SEQ ID NO:576 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 444 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION 1...444 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:576 agcaaacccc teegtattat cegeatagat gatactgege gaagcattge gagcagaceg caatgagcat tcatgccgta ctcggccaca tcttccagct tccaccctga gcacctacgc 60 cggggacaag caagaaagcg tccggcagat ctcgcgaata tctttcagca tggaggcctg 120 cgtagccccc accacaacat cagttgaccg gcattatccc acgtctggct gatacgaata 180 acgcgtcgaa aaggtattct ccatcggcat cgcgcatcat ttgaaagtct tgcgaccttt 240 gttcgaggtc agtgccagaa gcaccgtgaa cttgcctgca taatcangaa agggctgatg 300 ctgtcctctc ccatataagg agaaacggtg aggcatccac cttgagatgc tcgaagaacg 360 aacgggcata catatcactc gatt 420 444 (2) INFORMATION FOR SEQ ID NO:577 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 384 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: UNKNOWN (vi) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION 1...384 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:577 aggagcagtc ccacaactgc aagctatgcg acgtatgtct aaggagaaag acggagaact gcaccatcat gaagtggacg acttgctaca tttcctcggc aacgtttgac cgaagaaaca

ccctacgtac tgattgcgga tatctgcgag aactgcatca ccatcccgac gtcgtgctca

aagcaatacg cttcgtatga aagaatcctg gcagtactcc actgatggtg ataccgtctt

60

120

180 240

cctgagcaca aacttcccgg aggactgaac ctttagcccc cgcctcgctc tcccgctcta 300 cagattgcac cttctccaat agaattatag aaacctttgc aaaagagaag attatcaaga 360 aggtatcttt tttgctcacc tatt

- (2) INFORMATION FOR SEQ ID NO:578
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 540 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi.) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...540
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:578

ggagaaagac gatgccgtat tcggcaccac cctactgcgc aatgccatct caacggacag 60 120 gaatategee atateateeg tgaaaatetg ateaactgga agtggatege atageggaea tggatatget gateatgeaa etggetaege egagetgete eactteeega atatteeggt 180 240 cttggtaacg atcaataata catcgacctc tccaagctgt tcagtacacc caagagcgga 300 acgttgtaaa cgggttgctg gatgctgtgg tcaaaagtct cagagagaaa ggcaactact caaataagag caggggcaaa acagctatcc cccagatttg acaatgacag acgacaaaaa 360 420 gattcgggca gccatcgtag gctacggcaa tacggtcggt atgccttgca agcgcttaga 480 gaagetecag attttgaaat accggcattg neegeegeaa teegeegagg tteeettega geteageett eegtgtagta teegacateg ageactegaa teggtegatg tgeettggtt 540

- (2) INFORMATION FOR SEQ ID NO:579
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 535 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...535
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:579

ggcgaatcgg	tttcataaca	atgagaccgt	tgcacaaaaa	cccttccacc	cctcatatca	60
				gcttcatgcg		. 120
aaacctcaag	aataccccga	tggaaactgg	gaaaatttct	gtttgtttgg	tgcccatatg	180
				tctgcggcaa		240
tgaaatccta	taaaatagtt	gcaaacagct	gatagttagc	gcattgatgg	gagctaatca	300
gctgacaatc	gtttcttatt	tctcgcctat	ttgacgagga	aagagtactt	ctctaatgga	360
aacttgggga	aatttctatt	tgctcggtgc	cctataccga	aggtttgacc	tttcccgaag	420
acactaagaa	tetgetetge	acaaaagaac	tcaatgaaaa	tecectgeaa	cagtcttaac	480
agtgcaagag	cgaaataact	aaatatgttg	tgttatgaaa	agggagctat	atcag	535

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 667 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...667
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:580

ttatcagaac	gagcaccgta	cctcagactt	ctttcgagcg	tgctattatc	cttgctagat	60
tatttcggac	agcagggtat	ggggcaaggg	cgtaagttcg	ttttaagcaa	cccgtcaagc	120
ttctagactc	tacgaccatt	accctttcct	tgccctatac	gattgggcta	aatacacaca	180
tacgaaggga	gctgttagct	tcatacactc	ttagacttca	agactctgtt	gcctgaatat	240
gtgcaattag	tgatggtaaa	ggacatgatg	gcaagatggc	caattctatt	cctacccagc	300
aggaagtatc	gtcgtggctg	accgtggcta	tgctgatacc	gcctgctcaa	tagttgggac	360
agcacccaag	tgagttttgt	agtacgccac	ccaggtcctt	aaaatatgag	gttattcaag	420
agttggaact	cccagaacat	ggcatcagca	aatactagta	gatcagagag	tacggctcac	480
aggcgttcag	cgcaaggcaa	gtacactaag	ccattgaggc	atattgccct	ctacaacgaa	540
aacatggcga	tgtcgttgag	ttattgacca	acatagacac	ccttgcagaa	gtagtatagc	600
cttgctgtat	cgttcaagat	ggcttatcga	gattttcttc	ggaatttgaa	gcaacgcctc	660
agcatga						667

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 498 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...498
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:581

gtocoogott otoaggaogg acagooggoo tacatoaaac gaatocatoo ogaogoaatt 60 atatcatcag gcgagccagc aacctctcga aagagtccat atactgggag ccaatttgga 120 tgctgccgtg ctggtctgta ccatcaagat ccggtgacta ccaccgtctt tatcgatcgt 180 ttcctcgcta cggcagagcc tatcgcgtac cggttattct tgtattcaac aaaatagact 240 gctatcgcaa gaagatcgct tgcaattgga ccggctgtcg gctgtctaca ccgcataggt 300 tacccctgct gccacgtgtc ggcgattacg ggcgaaggcc tccggatctc aaatccctac 360 tegatggeaa getgacaete ettgeeggee ategggggtt ggeaaaaget etttgateaa 420 tgccctgatt cctcatgccg attgcgcaca gggggctata tnccaagccc atcataccgg 480 498 cattgcatac accacatt

- (2) INFORMATION FOR SEQ ID NO:582
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 508 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...508
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:582

60 gtcgagcaat aggataccta ggctctggct ctgataaacg gtgaactact ggcttcggag ttttttcgta tccggatgcc gtaggtttct tctgccaatc tacaagtagc ttgtaggctt 120 gatgccctag ttcttctcgc ttgagacact cttgaggaca cgattctctt tacgtagctg 180 ctctaactct tcttttcgtt caggggtagc tcactctggg gggattggga cactttcatt 240 gggacggatg aactttatct tcgagtccaa atttactaag ccaagagcga atgaaccatg 300 acttagacca tatttctgct caatggctac tttgctatct gacccgagag gtaatcctca 360 aggatgetaa ggegtteaaa gttgtttaaa tgttgeeeat aatggataet ggttgeatee 420 480 egeceaactg teaacttttt tagtacaegt caactttett etgatttgtg gttegaettt 508 tcctgatgga cgaacgcttc ttcttcgt

- (2) INFORMATION FOR SEQ ID NO:583
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 486 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...4\overline{8}6$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:583

gcagattcgc ggaaagatgc aatgcgaatc cgagctggtc	tctgtacctt aaaagtaatg ccgatcaacg gctacactca ccggcaccaa	tatagatatc atatcagacg ggtnaaggca tgaccgacaa	tgaagttggc aaaggacaat gcacacttcg ggcgaagttg	gccttgtctt cattgcccgt ctcgatgctt caaggaggtg aaatcataga	atacggetta acagaaagag gagteggatg etteegtaat gacagtteeg acaageeett aatatgeeta etcagggega	60 120 180 240 300 360 420 480
------------------------------------------------------	--------------------------------------------------------------------	------------------------------------------------------	------------------------------------------------------	--------------------------------------------------------------------	--------------------------------------------------------------------------------------------------------------	-----------------------------------------------------

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 530 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...5\overline{30}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:584

caagccgaaa tcctcggaca cttcggaccg cttctctttg ccgactatat ggcgtttgcc	agctggtaca cgattctcct tccatatccg ggggcggaca ccgccgcctg acacgcaatc	ggaatccgcc tgctgaacag cgatcttgcc tacaatgtgg ttcaagttgc	tcgaatggac ctctgtattc tctgcctgcg gagggggcga tcgtctcggc	gatctaccgc tgtatgccat	aagctcctat gaccaagttg ccgggtatta tggccacacg cgatacaaag tcggtttact ttccggacag attggaagcc	60 120 180 240 300 360 420 480 530
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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 734 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...734
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:585

getatgeett gettgatggt aggacaggtt eteettgegt eegatgatge aeceagttea 60 tgtatttcaa accacatcat atccctgctt ggcaaaggaa gacgggttgt gtgtcatctg 120 tegtgttgta tagattgata atetgetgge tateggatge aggggaatga atgattetae 180 tttcgtcttc ctgcggtaat ccgtatataa cgccgtccct cggccgtctt tcctatgtgg 240 300 tgcggtatag caattgcgta tcaacatagg caagccccgt aaaacaggag aagagaaagt ccgtcgagcc agttctttca acgggtcgtt ctgtggcaat ttagttccaa caactgtttc 360 agtteegett tgetgatgtg catacgettg gegggggett etteteatat tegaettett 420 ctaatggatt ggctcggata actcatggtc aacggcaagg taaaccaatc ggttcagcca 480 acaaaggcaa ggttggtctg cgatgctccg aagtttttgt atcgtttcag ataaaccttt 540 attecegtee gaacteeteg gtgatgteea agaaageaat gtegeteage ettttgaete 600 caaaaactct cgaatataac tttggtaata tcttgaattc tgtatgtgga gtttgagcct 660 atttccgtta getettactg caagacttet egeteeettt eteccatetg gaanttaaat 720 734 gaatgggaac tacg

- (2) INFORMATION FOR SEQ ID NO:586
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 492 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...492
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:586

60

120

cacggctttg	aggaattggg	ttttaatcct	gtatggtgca	attgaaatcc	gttacaaata	180
taggcttttc	tgtttgatgt	gaggagttta	cgaaaaggtg	aaacccaaaa	ttcagacatt	240
catagtgtcg	atgtctgatt	ctatgaaaaa	ccaaggggtg	tgacgactga	tatatttatt	, 300
gattatcaat	catttcaaag	atcgccggag	gttaatcatg	gcaaaggctt	gatgaatttg	360
ctcgagccga	cgcttcaaaa	gatagatagc	ggagctgtat	cgtgcttgta	ttatagaaat	420
atatccgttg	cagaacgctc	ttgccaatta	tttcttttc	caaccaacgt	tcttgtctgg	480
aagaaatatg	tc					492

- (2) INFORMATION FOR SEQ ID NO:587
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 363 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION 1...363
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:587

gcccgtaaag	tttccacttc	tcttggcaca	aggcacggaa	ggaattgctt	aggtttgaat	60
tccaaggtct						120
gagagtcttt	cgatctttat	cccgattccc	taccggtggt	atgatggatg	ccagccggta	180
caatgacggc						240
tcgtatctca	gcattaccga	actgccctgt	ggcaagacga	cgtcttccct	gatcantcca	300
ttctgaaagc						360
cga						363

- (2) INFORMATION FOR SEQ ID NO:588
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 396 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...396

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:588

ggtgccaagc	gtccgaagcc	cggacaggct	cctgccgcta	aaggtaagag	taagagccgc	ູ 60
				ataaggacga		120
				ttatttaaga		180
				cggcgggagc		240
				agacaatgag		300
				tgtagggtga		360
		gaaagaagaa				396

#### (2) INFORMATION FOR SEQ ID NO:589

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 390 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...390
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:589

ggcgttttaa caaca	agcagc gacaaagctt	tgcgcgaata	cattgccgac	gctgtcgcat	60
ccttgcagtg gtagg	gcttgc atggcaatgt	atttaagctc	atacaggtac	taagacgagc	120
gtactctttg tgcas	aaagtg ggacgagag	tatgcccacg	agtagaggat	tacaacatct	180
tetttgetac catgo	cagage caageaagga	a caatagtggc	gacaagattt	atcgnagcac	240
cactacgagg aggg	cgagaa tgttccttt	g cttgacaccc	acgggcatct	tatcttaagc	300
acgatetttt caace	cacgat ggactgacco	g aagatggcat	agcnaagcct	ttgcagagtt	360
	gactet etttttege				390

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 520 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature

# (B) LOCATION 1...520

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:590

ggctcgcgga	aatgaacttg	gtcgtctata	cateegggga	atagecteaa	ccgctacact	60
ctatgacttc	atcaacaaaa	agattatcat	coacaataa	totageeteau	taatacggga	
~~+~~~		·	cegegggege	teteettega	taatacggga	120
gataaatgeg	ccatcaatca	tcaccgaccg	gggaaggttt	ttccctcgtt	ggtgataagt	180
gcgttgcgaa	gaagaatttc	atctctttcg	tactattttc	ttttgggaaa	tcctttgaat	240
aaqtqcaqta	gegtagettg	atcacacaca	taaaaaatta	2000000	gaaggttcat	
+++		Lieucgeeeg	caaaagcccc	accyaaaata	gaaggttcat	300
tttcgacgtt	cccaaaacac	gattgacgaa	agtgatgggt	atcctttcag	gegaaateeg	360
agacaatagg	ccgtgtattt	catctcgatt	tgaaaggta	gagattana	* - t t	
200mat t		- a coogace	cgadagcgca	gecercyaaa	iglacegaat	420
caagatcaat	ggtttcaaga	attcgcggcg	gtagcaaaca	aatccggcag	tegtategea	480
tatattcatc	aggtcacgag	acccacatat	nangatasat	23 3	9-99	
	aggeodegag	acgedeatat	nengatgegt			520

# (2) INFORMATION FOR SEQ ID NO:591

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 582 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...582
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:591

aatcctcgtg	gaacggtcgg	ageggteteg	cttcaacgac	ctcttccacq	gagcggattt	60
acciccgata	tggaagactg	ggetttetee	tcggagaaaa	tcgactacgc	gtactcaage	120
actitigacet	gaaaagcctc	aaaggttcgg	gctggaagag	ctttcgatgg	cagtaacggc	180
ayccggagcc	gtactgacta	tctcgatctg	acacagcacc	atcagctaca	acacatcaca	240
cegetageeg	actggatgaa	aaccggtatg	tacgcttgga	taagttcacc	gtccaagcct	300
cyaattgett	agcccgatga	acgagggagg	caagagtctg	ctcacatcat	cgaccatacg	360
acaacgccta	rgggagcaag	gcgtatacga	catggatcgt	attcccactc	aaggaccctg	420
cacgcataca	agcccgacag	cagtggtgga	gtttttcttc	cgacatcctg	aagagcgagc	480
cateattgee	aacatctgac	agagataggc	gacttqqaac	gtttggtgac	gaaaggcgca	540
tgggacgcat	ttctncgcga	gaaatggtnc	actacgtgtc	gc		582

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 523 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...5\overline{23}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:592

gaggggtgat	agtgggaata	ccactcattc	tttqcaaaaa	attaagtgca	atcgttcggc	60
ttaanaan	accountage	tgccttccac	acgcaggata	cttgaccgcg	ttttacggag	120
ccycaacaaa	atacatacco	agtccaatca	caacttcaaa	togttogaag	acacggcgag	180
eegeeaceeg	acacacaggg	tgccatcagc	cttcattacc	attgtggctt	gcaagctcct	240
ctacctccat	googgaacga	ttggaagaaa	tatatacata	ggcaatgtcc	tctgaattgc	300
teegatgggg	gataatggca	aaagcatttc	ttcatcactc	atacttaaaa	gtgatgaggg	360
cagatcgatc	aattttteea	tatttaggg	togggggg	agatataaga	agaatactta	420
tattacggat	gtttatttgg	tatttcccgc	-cacetnata	gggtgtttta	ctttctcaac	480
cgataggctt	ngctcgtatc	ggatagtctt	ecegatilaty		0000000	523
gagctatcgc	ccccgaacga	tgagctgacc	cactgtcage	aye		323

- (2) INFORMATION FOR SEQ ID NO:593
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 524 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...524
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:593

				catacaccaa	tagtgctcgg	60
qcattcgtga	agttggatgc	atcgttaccg	gtegaagatg	Catacaccga	cagegeeegg	
atgrataatt	aggatoctgt	gcgcataccc	agaaagtcac	ttacctccgt	taggcaaatc	120
acgeacaace	ugoutous		~t ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	ctataccacc	aagaccgaat	180
caatgccggt	gttatcagat	agttgtcggg	graayaaccc	Ccacaccacc		240
gactctgaat	atacacacca	ttgctattgt	agccagcgat	tccgggagca	tttccaggct	
4 <del>-</del>	at an agat	ctgcatcgat	catcttccat	gaggcaggaa	taccttttcg	300
tccagcatgc	cegteacegt	Cigcalcyac	cyccccca	949944994	++	360
aatgattcgg	aaagtgtagt	tgttccggga	ttcggatttg	gateggatti	ggacciggac	
	attadatada	tcccacttaa	gettaettte	tagccgactg	cactaccggt	420
teggggtace	accaggegea	· · · · · ·	900000	++++	agatacette	480
caggttctgt	acaggagcaa	atcattggat	ccttctaccg	taacgtettt	acataccttc	
qqaqatacgc	ggctgtgtac	ttaacttcca	cgcaatactc	atga		524

- (2) INFORMATION FOR SEQ ID NO:594
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 493 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...493
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:594

ggcgagcttt	ttcacgcaat	tggatcangc	tcttttactc	tttccagtta	aaactcatat	60
tcttttctaa	atagttaggt	ttgctatttc	atgacataag	gcatactcgc	cggaaagcag	120
tcggcactgt	ccggtcgccc	gtagggtgtt	actattattt	atgatcacat	acctcggtca	180
gcacacccat	agtactttcg	ggtgcaagaa	accgatattc	aagccctctg	ctcctttgcg	240
agcttttcgt	cgatcagctt	aatgccttta	gaggcggcat	cggccaatgc	ttcgtggcat	300
cttccacaca	aaaagcaatg	tgatggatac	cttctccacg	ctttctatga	atttggcaat	360
agggctttcg	tcagaggtcg	gctccaacaa	ttcagcttgg	tctgccctac	catcataaat	420
gcggtacgca	ccttttggtc	ggtacttcct	caatgctgta	acacttgagt	cccaatacat	480
tttcgtagta	ggg	•				493

- (2) INFORMATION FOR SEQ ID NO:595
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 391 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...391
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:595

gcatcggagt	caatcatggc	tctctgtccg	aacgtatgct	tacgcgctag	gcgatacggc	60
tgaaggcatg	gtacaaagct	gcatggaata	cctcgatgat	gccacgaaca	tgagttcgac	120
gatgtggtga	tctcgatgaa	agcatcgata	ctttggtcat	gacagcagct	gtacgccttc	180
ttgtggaacg	aatggagctg	cagacatgca	ctatccgctt	cacatcggtg	tcaccgaggc	240
tggcgtggtg	aggacgggcg	gatcaagagt	gctgtcggca	taggttcgct	tttgctgatg	300
gcattggcga	taccattcgt	gtttcactga	gtgaggatcc	ggacatgaga	ttccggtagc	360
ccgcaaattg	cttgcctata	tagagaaacg	t			391

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 531 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...531
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:596

60 agegeagaag ctatgeeggt aeggtatett atetggetee teettteatg aaaegegeat gaggggtcaa gtaagcgagt tcctcagctt gacggataat acctggagca ggacaacgat 120 gataaagccc tgtctctccg catcaagctt tggccgtgaa gaacggctac catcgggatc 180 tgaaactcga ctccatcttg acaaacctta tacacgtgag caaatcatct ctctttccga 240 ctttgcgaag aacttgctgt cagcaagatc ccgggtggta tgtacaagac aggcttatgt 300 teeeggaaga aaagateege tetteegtga ageatattge taegateeta ttgettatge 360 420 tttggccgct atcgaccgtc agcgtggacg ctcacacagg agcagcaaga tagcgaacga 480 ttctttacca accactateg tgtcctgccg aagcactggt agagegttac cttggacgen aggoggtaga gtgaatgcag cattgactac gctgggtgta ctgtccagcg a 531

- (2) INFORMATION FOR SEQ ID NO:597
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 743 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: UNKNOWN
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
    - (ix) FEATURE:
      - (A) NAME/KEY: misc feature
      - (B) LOCATION 1...743
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:597

ccgacagcga	ggatcgatca	tggctgattt	tcggcgggca	taacttccca	gaggagaaag	60
acaaggtgtt	ctctacgctt	ggccaaggct	tctatggcgc	atccgtaaag	gtctcccatc	120
catgcccttg	gtggctaccg	gcctgactgc	acgaacagta	agcgtggcat	tgagcagtaa	180
tactccttgc	tctaccacgg	caaaagactt	cctccatcta	tatgagccgg	ctgtccggta	240
tcggtcgaat	ctcttcgcag	atattgcgta	aactgggagg	aatgggtata	ccggcggcac	300
tgagaaagcc	aacccttcgg	cttgcccggg	ttcatgatag	ggacttgtcc	aagaataacg	360
actttgacgc	ggtcgaaagg	gcaagtgtca	aagcccgaaa	aataaatcgg	gccggggggt	420

aaatcggact	ctgccgata	ttcacgcac	aaagtcggtc	agcttttcga	aataaaattt	480
atcgaattct	cctgtaaaac	ctttttccat	ccggcttcga	ttcgtacctc	tttcatgttt	540
tctgtttatg	taacgtgtat	attgtctttc	aaggacgggg	ctttacttga	aagcccccac	ູ 600
ggtagctgtc	cggcggggtt	ctccggtcaa	gtcatgggga	acaacgctat	gatagcagga	660
teggetttee	ctacgaatgg	ggcattggca	gaggatgata	gtcgtagcgg	aagttgtact	720
tctttttgat	caagtgtacc	cta				743

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1001 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...1001
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:598

tocatagott occaagogoa agaggttgaa gogtgaagoo gatgttgogt acaagooact 60 120 accaaagcca gattggaaat taccgtcggc accaaagcaa gagcaggata ttgccccatg aagccgcgtc ggaagaggag ccacttcccc tgtctgacca ggacgttgat caggcaaaaa 180 240 cetgeggetg egacgagaeg tagaaegtea geegeegtee eggeatgatt eggateegge 300 tccgatgaca aagacgatat agagggcata gcaaagcgcc gagatggcga ctatacaaag 360 ceggtaagee ctaceegate geceeteee gtaaggeeea teacaggeee aegeetatea 420 gggcgatgaa aatggccgtc aatggcacgg gcaaagtctt tccccaaaga aaagaagcat 480 cagageegtg acgaacageg gtagaggaag tggatggtgg tggetacace getggeeata 540 tagccatagc gtgaaagagg aaaagtgccg tgccggcata caagaagccc agcaataccg 600 eggeeetata teegeaegge tgaetttgaa getgeegeee gagaggegtg eagtataeeg 660 atggcgatgg ctgcgaagaa aaagcgatag aagagaaaag ctcgaacgaa gcaccettag 720 ccgaaaccgg cagcgtgaac agggggtgag cccgaatgtg gcggacgaca gtataccgac 780 cgcaagaccg tagagcgtga agatgtcatg aatgctgccg taacgaatat tgaggattga tactataata ataaggtata gcaggacgaa accgtaagcc gcacggagaa gacgaaagac 840 900 gatatgeeeg getettegae tteeeteeee etegtetgee ggetgeatee ggatagaggg 960 eggetegtea eteagagtee tgteegetge eceteetete ttgteggaga ggaggeggeg 1001 gcaggaaact gatcagttgt catcgaggcg aggaactccg g

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1274 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION 1...1274
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:599

tegeettgge	accttcaatg	gaaatcgcgg	tgtttcatct	cccctaccag	ttctattccg	60
aagccttacc	tgactgtgca	tttggaattc	cttcttggca	tccttcatag	agcatctcat	120
ccaagcgaat	caccgaaggc	atccatgatg	caccagttcg	gctactttgg	atcgagtgag	180
atcctcgggg	ttcagtcgta	ccattcgagc	agagcgttgt	atgcccagca	ccattcatag	240
togtatatog	gctatgaatt	tccttcatcc	gctcattcac	ctccgcaagg	ctttgatctt	300
gccttctttg	atcaaggagg	caaggcggtg	gatctgttgt	tgtgagcgat	catgccacag	360
atgtccaccc	agctgccgtc	tccctcattg	tggtcggctt	gagagcactc	agcacctcct	420
catccgtacg	gcaaggacaa	tttcaaggcg	tttgatgatg	gaattgccga	aaaacttgtt	480
cagococato	catagaacat	cagccccttg	tccaaggcag	aagaacgtat	gcgcatatct	540
			gtatcttgcg			600
geogegeate	atcttgccgg	cagtgaaagg	actcaaggat	tgaagttgat	attgtccagc	660
aaatccggat	ctttacgctt	atctctgccg	gccacttctt	ggcgtcacga	atcgtcccca	720
cactgcgcag	attgaacccg	gtaccaaata	cgattcgtta	cggtcctcta	tgatataaga	780
gaagggaagg	ccgagctgtc	aatatggtgt	acgtgtcgac	ccatcaccaa	cgtaaaaggc	840
cctattctqq	atggccaaag	gatataagag	tegetegtgg	tctcgagccg	cgctccacga	900
tgccctgatg	gatggggcg	agettgtaga	gtgattgctc	tggttagagc	cgctgccggc	960
attgaggaaa	gagtatagac	ggcaatgagc	aggctcgact	tgtgcatcga	cacggtatat	1020
ggcccggcaa	gacggcacag	gcctcqccqt	tttcgccttg	gcagttggca	aagaaaagga	1080
atcatgtgca	gagaaaaggt	gccccaaatg	agtaccctgc	cctacaaaca	gtgcgaaacg	1140
gtagcaccat	ccqtaacqct	gctgcccgaa	cagagatgaa	atcgcggcag	acgacattgt	1200
agectacega	cacqqqqqcc	tetttttget	attgatactg	ccgttgcaga	gatgcgaggc	1260
acceggtgat		•				1274
23-3	-					

- (2) INFORMATION FOR SEQ ID NO:600
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 587 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...587
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:600

ggctccgtat aggttgtgat aacaccttca t	taattgcgaa	gaaccacatt	cgtggggact	60
gagatacaac atagttegge attacaggta t				120
aaaggtagga acagcatagc ccgaggttgt c				180
ttagataccg gcgtgcgaaa tgacctattc c				240

aaggagcaca	cgcatcttta	ccagcaaatg	taccaatctc	ttcatcacat	gtgtcaatca	300
					ttggccattc	360
tttcacaagc	ctctactgct	tctttcggta	actcattcgg	gtggttgaag	tgagtgttca	420
gccacaccgg	atgatatttt	ttgagcatat	ccaccaattg	aggogttata	cactaaaaaa	480
					tttgcgcagc	540
gctttcatta	tggtattcca	agcgttctgt	cgctgacaag	gagggca		587

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 672 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...672
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:601

gagaaageee ttgtcatget gegagaaace ateggategg agettteeea ttgcatacat 60 gatcacattt ctccctctat gagacctaag cagtggataa gaatctgatc gtattcctac 120 ccctgttttt cggacacagg attggtgtac ggaagccttg ctaaggctga ccatactcct 180 gatageattt tgttegeate gagtgeagte tatetettea atgatatttg egatagageg 240 atogaogoot goatocogto aaatogagao gooctattgo cagoggagoa tggatototo 300 caaagettat atactgatag etetgettgt ggttttgget tgeeagtgat attgteacte 360 cttgatttcc cttttgccgt ctatgccctg attctatagt gctttatctt ctgctgaatc 420 ttttctattc actgaaaggc aacacattcc catcgtggat gctttcctcg tagctttcgg 480 ctttctgatc gattgtatgc ggccggagca gtgagcggag tacccatttc ccattggttg 540 ctttgatgac getetteeta teettgetge tegeettegg caagaggaag aagaeetgeg 600 tctgctgcag gagacggctc tttcatcgcg tcctgtctca aacattatac ggatggattc 660 cctcaatgtc ct 672

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 541 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...541
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:602

tcctaaacct	ctttccgagc	aatcatctga	ggggtaaata	tgacagagaa	taaggtatta	60
	acatatattt					120
gaacgagtct	tttcttcttg	atacaaagtc	cccgaaccta	ctctgaggcg	tetteeetgg	180
	acgtccgctt					240
	gtaggagtgg					300
	cacgggtagg					360
	gcaccaccac					420
	tegggtttge					480
	tggacactaa					540
a						541

- (2) INFORMATION FOR SEQ ID NO:603
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 483 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...483
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:603

ggcgacgccc	ccgaacagaa	taccggcgga	ggcgatacta	ccaccacgaa	cggagtggag	60
gcgacacgcc						120
getegaceeg						180
cgcaaaaaga						240
gaaggctggc						300
catcagcctc						360
gcggttgaaa						420
gagatacata						480
gct						483

- (2) INFORMATION FOR SEQ ID NO:604
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 512 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...512
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:604

tcttcttcat	cagggctgtc	acttctgtat	ctttctcaag	aaggaattct	acggagcttc	60
gatattctct	ccgttcacca	ttaccttgtc	cacttcgtac	cttcggcagg	gatgggatgt	120
attttaatac	gacggcctgc	cactaattgg	aaccgctgtt	caggggctgc	ccatcggccg	180
ttagctttat	ctctcctttt	cgggctggat	gaccactacg	gaatatacag	agataggttc	240
ataaacgctt	ccacttcatt	tgtagattct	ttgactacta	catgagtata	actgttttga	300
agggtagtcc	tgaaaaatcc	acataatctt	taagtccgaa	ataactaaat	ctgctatgga	360
aggctttggg	aagaatgtct	ctgaagcgag	cattctttgt	cgtactcata	gtagtaccag	420
aaatcgtcac	gcccggcttt	gcaatatcca	ttccttcact	gtcgtattcg	tatatcaatt	480
caaattcgtt	aaacctgtac	tggccgggga	tc			512

- (2) INFORMATION FOR SEQ ID NO:605
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 666 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...666
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:605

cggccatagc	gtagggctgt	ccgtccgcgg	agtccgcgag	tgggtgcgtt	ggctcgtcgg	60
aataccaatc	tggagatagc	actcaagaac	aagtccatgc	atacgatcgt	gccgaagcgc	120
ggctgcgttc	tttggaacag	ccggtttttt	ccacaacccc	ggcacgggag	cgaaagcgga	180
aaacgcacct	tectetete	tgtcagtcca	caaacaaacg	aatagtcatg	cgaaagaaac	240
gctccatccc	tactacaaag	tcagcaggcg	gaagttcagc	aaacgaaatt	ccggcgcaga	300
tattcgagaa	agaggagaag	aaacggacgg	cgacgagggc	tgagatcagc	ctgctcctcc	360
ttgtcgccct	cggtatctgg	atagccaagc	gaacagggct	tggttcgttt	ctccggccga	420
agtcgcctac	accgttccgc	atcgaataga	ccaggctcac	cctgacaccg	ggtgaggatt	480
tecttaceca	aggacggtca	gctggcggtg	cgacaccctg	ccgcaagact	cttggctggc	540
tatcgctctc	cggacggagc	ggatgcagat	accctgctga	tctcgctgcg	gccgagggaa	600
aagaagtcgt	cacccgtgcc	ggacgcaact	actattacac	gctaagataa	acggactcaa	660
gcccgg						666

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 406 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...406
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:606

caaagagaaa aggcg	tgtag atggtatgco	tggcacacga	tctacacgcc	ccggagttat	60
tegettetga gateg	togag tacttogtog	, tacttgtccc	gatctcttcc	accatatctt	120
eggtgattee etteat	ttttc ctacggtctt	ctggtagcga	ttcttggctt	cataatagcc	180
ttccaccacg ctatco	cttac tttgtcggct	gtactgttga	tgtcttcaac	gaagcgagta	240
cgctttcacg atcage					300
qaqaqaaaac tttcc					360
tcaattttqt cagaa					406

- (2) INFORMATION FOR SEQ ID NO:607
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 519 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...519
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:607

cgccgaattc	accaaacgtt	tccaacgtat	caacgaagca	catgggctgg	tcagcaactc	60
				ggatatggcc		120
				gactttactc		180
				atacgcttca		240
				tttcttctgg		300
				cgacggatct		360
				ctcctccgtc	_	420
cgcaaaagca	aaagcaaaag	ccgccattct	tagcgacaag	gattacactt	aaagtcggaa	480

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 664 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...6\overline{64}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:608

agcagattat gccatcacgg cctctcactc ggagggtttc ggtctgaata tctggaggct actgettgtg gaaaacccgt tgtagccact gatttgcccc attcagagaa atctgcggca 60 caggetttca ggacaacgaa ttgttttttc tgtaggaaac caaaaagaat tggaggattg 120 catactaaaa agccttgtca tacgttcaac cctcaaaaag tctccgatat caggcatcat 180 ttctcgcgga aacaatgtct gtacaatatc agaactatta tacggagcta tcagtccact 240 aaaatgaatt caatgaagag tgcatgttcc gattattact gctcaatcgt actttataaa 300 agcaaaccgg atattattcg ggatgtcatt actccttttt ctctgatacg gtaactaaga 360 agaagettat ceteatagae atteteegae tgacagtett egtgteetee aagaagaaag 420 accggaggat ttcaggtatt tctttaataa ccgcaatata ggattcggat cagctcacat 480 atoggtatta gagaggoago togottoaat cottottato attaattota atootgatgt 540 gcagtttggc cctgaagtgg tgccgacatt ggcttcaaca tggaccgaga atcctgatat 600 agga 660 664

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 476 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...476
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609

gggcatcacg	ccttccacaa	caacgaagat	gcatacqaqa	agcatttcgt	gcgttggaag	60
aggcaaatag	cttgccaaat	cgaggaaatg	aaaagtcgtc	gtagagetta	aaatgatgcc	. 120
gatateette	actacataat	ctgtttgatt	tatttgtgga	atgtgcagag	cgacacgatg	180
tccgaaattt	gctgaaataa	tgtacctttg	ccgcgctgat	tattatcaaa	tagtgccgaa	240
conttoattt	tcagtgcgtt	tttqtccqag	aggagcagcc	cagtgtccgt	gcgtaagctc	300
ctgatgcacc	ggccgaatcg	acagaaaaga	tgatcgttca	ccaattacta	acaacaaata	360
atacaagcag	tggatacttt	aagcttcaag	acatttctgc	gaacaaaagc	aactgttacg	420
aaggaatggg	tcattgtaga	tctgaaggac	agacacttgg	ccgtatgtgt	gccaag	476

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 775 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...775
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:610

60 gggtaacgac agcattette accggatega teatttggge aatageetgt tgaatgette 120 cagaggaacc tgaggagcaa aagcattcac cgtctgattt ccacctcaat acccgggata tagccgccat cggtgaagta ggtggagatt cattggcata agcattgttc ttacgcttgt 180 240 ctctttcgtt gtattgttct cgtatcgctt gagcacattc gngccgtgca cgatccgtat 300 tegeettggt gaatacegaa etgaeggagg etttetatet etgeeaceaa tgegteateg 360 ctttctccgc ttcaccctca cgaaccgagg caacaaaatt gaagcgtcct tagtctgggt 420 gatgtacatg aagttagaga agaaagctcc tgactgagga aaggagcgtt aggcttgtga 480 gtaatctcgg acagacgctc atcacggctg tagtgatcac ctgtttcata tagtcttcca 540 caagtccgaa atcgatcctc gcacttcttg aggagtgggg tcgctcttga agctgatggg 600 agetgegtgg tagtageete ageateggta geaatggeta egataggeea tegttgteet 660 ctaccggcgt atagatacgc tctgctggat tcacggggca ggaacgtcct tgaagagttc 720 tttgatettg ttetecacat agtecaateg atateteeca egateaceag acettgeagg 775 tcgggacgat accattctta taatagttgc gcagctcatc atgcttggaa gttga

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 833 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION 1...833
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:611

cegaagettg ttegtactee eggaaentge acaegggget tatttetgea gaegggaaag 60 acgtgcaggt gttcgaccgg gcagaagacc atcccgggcc gagtaccgat ttctttcggg 120 caccategee egegaageeg gegtegtetg gtgettetee etettegaga agegegetee 180 cgggctttac cacaatcggc cgtcgtgctg gagcgggacg gcactatcgc agggaagtat 240 cgcaaatgca catccccgat gaccctgcct attacgaaaa gttctatttc acaccggcga 300 cttgggcttt acccccatcc cgacgtccgt cggatgcctc ggctactggt ttgctgggat 360 cagtggtatc ccgaagcggc gcgactgatg gcatgcaggg tgccgatata ctcatttacc 420 ccacggccat cggtaccgag atacggacct gcctgccgag cagctccgcc aacgtcaggc 480 gtggcagatc tacagcgcgg acatgccgtg gccaacggta tttccccgtg gtggctggta 540 acaagggteg gecaegagge agaecettea ggeegeaeeg gtggeateeg ttetgggget 600 ccggattcgt agccggaccg cagggcgaac tgctggcgag ctgagcgcaa cggaagaggc 660 ggtggaggta gtggatatag atccctccga accgagcagg tgcgccgctg gtggccgtct 720 teegggateg geggaegaeg ettteteegg eettaeggan egttteette geggetgaee 780 atcaggcgag aggggggatg gcgttccgtc ccttccccct ccgacaagga gcc 833

#### (2) INFORMATION FOR SEQ ID NO:612

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 469 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc_feature
  - (B) LOCATION  $1...4\overline{69}$
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:612

tggttcgctg	ccccaagtcg	ttgtacgatc	gtcttcgcga	agaggatagg	cgcgtttccg	60
agtacccgtc	gatattctgt	ccgatgagga	cgatacggcg	gtacggaaga	agaccccttc	120
aaaaacacgc	tggtcaggca	tcaggatgct	tcccctactt	cgccttgcga	tacttcgatc	180
tgaagaaagt	cttcactccc	tccgcttcca	tatagatttg	ggcacctacc	acttcqccat	240
atacagaaga	acatcggcga	gcagccggaa	gaccgccatc	tgacgcgcaa	cctgacggct	300
teggeegaat	acaggatttc	gccgaggagc	atagacccga	agatggaagc	gtttggtgcg	360
ggatttggac	tacttccgag	accggcganc	aacccctata	tcaccccaaa	ccactccgca	420
ctatcatatc	gagaaaagaa	aattcgggct	gaagttccnt	gcccggaaa		469

# (2) INFORMATION FOR SEQ ID NO:613

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...975
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:613

60 cagtggtgat tttggcgctc tcttcaagtt gctccatttg ccgatggcca tgagatgctt ttcgtgggat gatcacagaa ttctgggtgt tttttatccc ggatttgaaa aacccgcaat 120 180 ggaatatcac tgggaagagg tcttcccgaa ctggactcga agaatccgat ggaccgtcgg 240 gagatggage agegteggag tatettegtg aaaaggeeaa agaageaget geataegegg 300 aaagacatet tetgtgegee ttgeetetge etetttgggt aegeaacege aagacageee 360 aageetgeea eteettteea gteecaactg aceggaatae tgeggaagag cagateeaac gcctgagcga aggcatagac aaactggctg aacaggcgaa cagcttgccc gtatcggccg 420 480 gactgcagcc gccatgacgg aagctacgag cagatgcaag cggatcagga aggcctgcgt 540 ctcaattcgc atcgtatatc cagcagatgg aaagcctcag tcgcaatatc tccggcctga 600 taccatatac gaaatacage teaagggeat cageteecag ategacacat egategeate 660 aaccgcggat tggctcatat ccgagatatg tatgacatag tgtcatcgac agttcttcat 720 tccgcaacga aaacgagcgt atggcagcca actgacacaa ctcaacgagg tgtatgctcg 780 cttgctccaa gccttacaac gaatgtaggt entaceeggt atgeceggna attttggtge 840 ttctatcctt catcatccgg cagctcaccc ttataagcca tggcagtagg ttcaatggga 900 atgccaatag gcaaaagatg atcaacctga tgtacctcgt gtcatcgcca tgatggcttt 960 gaacgtatcg agtgaggtac tggatggttt cacaaagtgg ataagagctt acctcttcat 975 cgacggtccg ataag

- (2) INFORMATION FOR SEQ ID NO:614
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 505 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: circular
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: 'UNKNOWN
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
  - (ix) FEATURE:
    - (A) NAME/KEY: misc_feature
    - (B) LOCATION 1...505
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:614